

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2003, 03:01:46 ; Search time 23 Seconds

(without alignments)
139.439 Million cell updates/sec

Title: US-10-033-067-1

Sequence: 1 MUKLTPLPKMKVSAALLCL.....ERWVDSMKHLDFQNLKP 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008
Listing first 45 summaries

Database :

Issued Patents:AA:*
1: /cg2_6/prodata/2/1aa/5A_COMB.pep.*
2: /cg2_6/prodata/2/1aa/5B_COMB.pep.*
3: /cg2_6/prodata/2/1aa/5A_COMB.pep.*
4: /cg2_6/prodata/2/1aa/5B_COMB.pep.*
5: /cg2_6/prodata/2/1aa/PCPUS_COMB.pep.*
6: /cg2_6/prodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	412	72.7	77	1	US-08-347-492B-9
2	412	72.7	77	2	US-08-421-144A-6
3	412	72.7	77	2	US-08-798-143-9
4	412	72.7	77	4	US-09-366-887A-12
5	408	72.0	76	1	US-08-480-449-20
6	408	72.0	76	2	US-08-716-188-3
7	408	72.0	76	2	US-08-660-542-20
8	408	72.0	76	4	US-08-479-603-20
9	396	69.8	74	2	US-08-615-232A-6
10	396	69.8	74	3	US-08-470-323-6
11	367	64.7	99	1	US-08-127-499A-35
12	367	64.7	99	1	US-08-482-847-35
13	367	64.7	99	1	US-08-347-492B-8
14	367	64.7	99	1	US-08-480-449-19
15	367	64.7	99	2	US-08-479-126B-5
16	367	64.7	99	2	US-08-421-144A-5
17	367	64.7	99	2	US-08-726-830A-5
18	367	64.7	99	2	US-08-660-542-19
19	367	64.7	99	2	US-08-798-143-8
20	367	64.7	99	3	US-07-927-391-24
21	367	64.7	99	3	US-08-995-156A-5
22	367	64.7	99	3	US-09-044-855A-5
23	367	64.7	99	3	US-09-044-855A-5
24	367	64.7	99	4	US-08-679-493A-152
25	367	64.7	99	4	US-08-479-603-19
26	367	64.7	99	4	US-09-419-281-5
27	367	64.7	99	4	US-09-366-887A-10

28	367	64.7	99	5	PCT-US96-10087-5
29	367	64.7	99	6	5212073-2
30	357	63.0	109	2	US-08-421-144A-7
31	357	63.0	109	3	US-07-927-391-16
32	357	63.0	109	4	US-08-679-493A-153
33	354	62.4	110	4	US-09-366-887A-13
34	350	61.7	97	4	US-09-366-887A-27
35	337	59.4	99	1	US-08-480-449-18
36	337	59.4	99	2	US-08-660-542-18
37	337	59.4	99	4	US-08-613-822-18
38	337	59.4	99	4	US-08-613-822-18
39	337	59.4	99	4	US-09-479-729B-18
40	334.5	59.0	96	4	US-09-230-637-44
41	328.5	57.9	98	4	US-08-613-822-4
42	328.5	57.9	98	4	US-08-852-212-2
43	328.5	57.9	98	4	US-09-479-729B-4
44	328.5	57.9	98	4	US-09-261-201A-4
45	319.5	56.3	104	4	US-08-744-419-2

ALIGNMENTS

Sequence 5, Appl
Patent No. 5212073
Sequence 7, Appl
Sequence 16, Appl
Sequence 153, App
Sequence 27, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 44, Appl
Sequence 4, Appl
Sequence 2, Appl
Sequence 4, Appl
Sequence 2, Appl

RESULT 1
US-08-347-492B-9
Sequence 9, Application US/08347492B
Patent No. 5602008
GENERAL INFORMATION:
APPLICANT: Wilde, Craig G.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Bandman, Olga
APPLICANT: Selthamer, Jeffrey J.
TITLE OF INVENTION: EXPRESSED CHEMOKINES, THEIR
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTED Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/347,492B
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/303,241
FILING DATE: 07-SEP-1994
APPLICATION NUMBER: 08/320,011
FILING DATE: 05-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lulher, Barbara J
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PP-0024
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: GT 126829
US-08-347-492B-9

APPLICANT: LEDER, PHILIP
APPLICANT: ROTHENBERG, MARC
APPLICANT: GARCIA, EDUARDO
TITLE OF INVENTION: EOTAXIN: AN EOSINOPHIL CHEMOTRACTANT

FILE REFERENCE: 00383/025002
CURRENT APPLICATION NUMBER: US/09/366,887A
CURRENT FILING DATE: 1999-08-04
PRIOR APPLICATION NUMBER: 60/000,449
PRIOR FILING DATE: 1995-06-22
PRIOR APPLICATION NUMBER: 08/522,713
PRIOR FILING DATE: 1995-09-01
PRIOR APPLICATION NUMBER: 08/522,713
PRIOR FILING DATE: 1998-06-16
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 12
LENGTH: 77
TYPE: PRT
ORGANISM: Homo sapiens
US-09-366-887A-12

Query Match 72.0%; Score 412; DB 4; Length 77;
Best Local Similarity 100.0%; Pred. No. 9.6e-45;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 QPDSVSIPTCCFNVINRKIPQRLSEYTRITNIOCPKEAVIFKTRKGEVCADPKERW 92
Db 1 QPDSVSIPTCCFNVINRKIPQRLSEYTRITNIOCPKEAVIFKTRKGEVCADPKERW 60

Qy 93 VRDSMKHLDQIFONLKP 109
Db 61 VRDSMKHLDQIFONLKP 77

RESULT 5
US-08-480-449-20
Sequence 20, Application US/08480449
Patent No. 5688927
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Botun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,449
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 27866/32779
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 76 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "Hu MCP-2"

US-08-480-449-20

Query Match 72.0%; Score 408; DB 1; Length 76;
Best Local Similarity 100.0%; Pred. No. 3e-44;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 QPDSVSIPTCCFNVINRKIPQRLSEYTRITNIOCPKEAVIFKTRKGEVCADPKERW 93
Db 1 QPDSVSIPTCCFNVINRKIPQRLSEYTRITNIOCPKEAVIFKTRKGEVCADPKERW 60

Qy 94 RDSMKHLDQIFONLKP 109
Db 61 RDSMKHLDQIFONLKP 76

RESULT 6
US-08-716-188-3
Sequence 3, Application US/08716188
Patent No. 5908829
GENERAL INFORMATION:
APPLICANT: KELLY, RODNEY M
TITLE OF INVENTION: USE OF MCP-1 FOR INDUCING RIPENING OF
THE CERVIX
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,188
FILING DATE: 30-SEP-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/00733
FILING DATE: 31-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9406463.1
FILING DATE: 31-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 117-219
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4091
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 76 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-716-188-3

Query Match 72.0%; Score 408; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 3e-44;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 QPDSVSIPTCCFNVINRKIPQRLSEYTRITNIOCPKEAVIFKTRKGEVCADPKERW 93
Db 1 QPDSVSIPTCCFNVINRKIPQRLSEYTRITNIOCPKEAVIFKTRKGEVCADPKERW 60

Qy 94 RDSMKHLDQIFONLKP 109
Db 61 RDSMKHLDQIFONLKP 76


```
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/615,232A
FILING DATE: 13-AUG-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9318984
FILING DATE: 14-SEP-1993
APPLICATION NUMBER: GB 9408602
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 550-32
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-615-232A-6

Query Match
Best Local Similarity 100.0%; Pred. No. 9.5e-43;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 DVSIVPTCCFNVINKRIPQRLSESYRTINICPKRAVIFKTRGKVCADPKERWVD 95
DB 1 DVSIVPTCCFNVINKRIPQRLSESYRTINICPKRAVIFKTRGKVCADPKERWVD 60
DB 96 SMKHDOIIFONLKP 109
DB 61 SMKHDOIIFONLKP 74

RESULT 10
US-08-470-323-6
Sequence 6, Application US/08470323A
Patent No. 6031080
GENERAL INFORMATION:
APPLICANT: WILLIAMS, TIMOTHY J.
APPLICANT: JOSE, PETER J.
APPLICANT: GRIFFITHS-JOHNSON, DAVID A.
APPLICANT: HSUAN, JOHN J.
TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
FILE REFERENCE: 550-33
CURRENT APPLICATION NUMBER: US/08/470,323A
EARLIER FILING DATE: 1995-06-06
EARLIER APPLICATION NUMBER: PCT/GB94/02006
EARLIER FILING DATE: 1994-09-14
EARLIER APPLICATION NUMBER: GB 9318984.3
EARLIER FILING DATE: 1993-09-14
EARLIER APPLICATION NUMBER: GB 94086902.2
EARLIER FILING DATE: 1994-04-29
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 6
LENGTH: 74
TYPE: PRT
ORGANISM: human
US-08-470-323-6

Query Match
Best Local Similarity 69.8%; Score 396; DB 3; Length 74;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 DVSIVPTCCFNVINKRIPQRLSESYRTINICPKRAVIFKTRGKVCADPKERWVD 95
DB 1 DVSIVPTCCFNVINKRIPQRLSESYRTINICPKRAVIFKTRGKVCADPKERWVD 60
```

```
QY 96 SMKHDOIIFONLKP 109
DB 61 SMKHDOIIFONLKP 74

RESULT 11
US-08-127-499A-35
Sequence 35, Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-35

Query Match
Best Local Similarity 69.4%; Score 367; DB 1; Length 99;
Matches 68; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

QY 11 MKVSAALCLILMATSPGLOADPSVITTCFNVINKRIPQRLSESYRTINICP 70
DB 1 MKVSAALCLILMATSPGLOADPSVITTCFNVINKRIPQRLSESYRTINICP 60
QY 71 KEAVIFKTRGKVCADPKERWVDSMKHDOIIFONLKP 108
DB 61 KEAVIFKTRGKVCADPKERWVDSMKHDOIIFONLKP 98

RESULT 12
US-08-482-847-35
Sequence 35, Application US/08482847
Patent No. 5556757
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
```

STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ. ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-482-847-35

Query Match 64.7%; Score 367; DB 1; Length 99;
Best Local Similarity 69.4%; Pred. No. 6.4e-39;
Matches 68; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

QY 11 MKVSALLCLLLMAATPSGGLAOPDSVSIPTCCFNVINRKIPRIQRLSEYTRITNIQCP 70
DB 1 MKVSALLCLLLIAATFIPIGLAOPDAINAPVTCYNTNKRISVORLASYRITSSKCP 60

QY 71 KEAVIFTKRGEVCADPKERWVDSMKHLDQIFONLK 108
DB 61 KEAVIFTKIVAKELCADPKRKQWQDSMDHLDKOTQTPK 98

RESULT 13
US-08-347-492B-8
Sequence 8, Application US/08347492B
Patent No. 5602008
GENERAL INFORMATION:
APPLICANT: Wilde, Craig G.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Bandman, Olga
APPLICANT: Sellhammer, Jeffrey J.
TITLE OF INVENTION: EXPRESSED CHEMOKINES, THEIR
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/347,492B
FILING DATE: 29-NOV-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/303,241
FILING DATE: 07-SEP-1994
APPLICATION NUMBER: 08/320,011
FILING DATE: 05-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0024
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ. ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: GI 487124
US-08-347-492B-8

Query Match 64.7%; Score 367; DB 1; Length 99;
Best Local Similarity 69.4%; Pred. No. 6.4e-39;
Matches 68; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

QY 11 MKVSALLCLLLMAATPSGGLAOPDSVSIPTCCFNVINRKIPRIQRLSEYTRITNIQCP 70
DB 1 MKVSALLCLLLIAATFIPIGLAOPDAINAPVTCYNTNKRISVORLASYRITSSKCP 60

QY 71 KEAVIFTKRGEVCADPKERWVDSMKHLDQIFONLK 108
DB 61 KEAVIFTKIVAKELCADPKRKQWQDSMDHLDKOTQTPK 98

RESULT 14
US-08-480-449-19
Sequence 19, Application US/08480449
Patent No. 5688927
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,449
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 27866/32779
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc-feature
OTHER INFORMATION: "Hu MCP-1"
US-08-480-449-19

Query Match 64.7%; Score 367; DB 1; Length 99;
Best Local Similarity 69.4%; Pred. No. 6.4e-39;
Matches 68; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

QY 11 MKVSAALLCLLLMAATFSPQGLAOPDSVSIPTCCFENVINRKIPQRLSTRTITNIQCP 70
|||||
Db 1 MKVSAALLCLLLIAATFIPQGLAOPDAINAPVTCYNTNRKISVQRLASVRRITSSKCP 60

QY 71 KEAVIFKTRKRGKVCADPKERWVRDMSMKHLDOIIFONLK 108
|||||
Db 61 KEAVIFKTIYAKKICADPKKQKWDSDMDHLDKQOTPK 98

RESULT 15

US-08-479-126B-5
Sequence 5, Application US/08479126B
Patent No. 5866373
GENERAL INFORMATION:
APPLICANT: LI, HAODONG
APPLICANT: RUBEN, STEVEN M
APPLICANT: SUTTON, GRANGER G III
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN MONOCYTE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,126B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,425
FILING DATE: 21-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05384
FILING DATE: 16-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0340001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ. ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-479-126B-5

Query Match 64.7%; Score 367; DB 2; Length 99;
Best Local Similarity 69.4%; Pred. No. 6.4e-39;
Matches 68; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

QY 11 MKVSAALLCLLLMAATFSPQGLAOPDSVSIPTCCFENVINRKIPQRLSTRTITNIQCP 70
|||||
Db 1 MKVSAALLCLLLIAATFIPQGLAOPDAINAPVTCYNTNRKISVQRLASVRRITSSKCP 60
QY 71 KEAVIFKTRKRGKVCADPKERWVRDMSMKHLDOIIFONLK 108
|||||
Db 61 KEAVIFKTIYAKKICADPKKQKWDSDMDHLDKQOTPK 98

Search completed: February 18, 2003, 03:06:35
Job time : 24 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2003, 01:56:46 ; Search time 70 Seconds
(without alignments)
207,490 Million cell updates/sec

Title: US-10-033-067-1

Perfect score: 567
Sequence: 1 MKLPLPSKMKVSAALLCL.....ERWVRDSMKHLDPQLFQNLKP 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A.Geneseq_101002:*

- 1: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
- 2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
- 3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
- 4: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
- 5: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
- 6: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*
- 7: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
- 8: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
- 9: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*
- 10: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
- 11: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*
- 12: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*
- 13: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*
- 14: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
- 15: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*
- 16: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*
- 17: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:*
- 18: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*
- 19: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*
- 20: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
- 21: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
- 22: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
- 23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	567	100.0	109	19	AAW42072
2	567	100.0	109	23	ABG35167
3	563	99.3	109	18	AAW26655
4	563	99.3	109	23	ABG35168
5	562	99.1	109	23	ABG35169
6	517	91.2	99	20	AA105300
7	517	91.2	99	20	AAV07233
8	517	91.2	99	20	AAV07237
9	412	72.7	77	21	AAAB15786
10	412	72.7	77	23	ABR80903

11	408	72.0	76	21	AAV69031
12	408	72.0	76	23	AAO21099
13	408	72.0	76	23	AAO21109
14	404	71.3	76	23	AAO78390
15	404	71.3	76	23	AAO68353
16	389	68.6	77	20	AAV14223
17	382	67.4	71	20	AAV07234
18	382	67.4	71	20	AAV07238
19	367	64.7	99	13	AAO28663
20	367	64.7	99	16	AAO73914
21	367	64.7	99	16	AAO70800
22	367	64.7	99	19	AAO40114
23	367	64.7	99	20	AAV48391
24	367	64.7	99	21	AAV6176
25	367	64.7	99	21	AAV15785
26	367	64.7	99	22	AAO87914
27	367	64.7	99	23	ABO80901
28	367	64.7	99	23	AAO52440
29	367	64.7	99	23	AAO77179
30	363	64.0	99	10	AAO95387
31	363	64.0	99	11	AAO63398
32	360.5	63.6	77	23	AAO78395
33	360.5	63.6	77	23	AAO68358
34	358	63.1	72	16	AAO70804
35	357	63.0	109	13	AAO24353
36	357	63.0	109	22	AAO27814
37	357	63.0	109	23	AAO21440
38	357	63.0	109	23	AAO52441
39	357	63.0	143	22	AAO12965
40	354	62.4	94	23	AAO78393
41	354	62.4	94	23	AAO68356
42	354	62.4	110	23	ABO80904
43	350	61.7	97	18	AAO14990
44	350	61.7	97	18	AAO10099
45	350	61.7	97	21	AAO15794

ALIGNMENTS

RESULT 1
AAW42072
ID AAW42072 standard; Protein: 109 AA.
XX
AC AAW42072:
XX
DT 09-JUN-1998 (first entry)
XX
DE Human MC proprotein.
XX
KW Human monocyte chemotactic proprotein; MCP; Incyte clone; allergy;
KW macrophage; diagnostic assay; body fluid; lung; biopsy;
KW autoimmune disease; AIDS; asthma; rheumatoid arthritis; NIDDM;
KW breast cancer; bladder.
XX
OS Homo sapiens.
XX
PN WO9802459-A1.
XX
PD 22-JAN-1998.
XX
PF 15-JUL-1997; 97WO-US12349.
XX
PR 15-JUL-1996; 96US-0683655.
XX
PA (INCYTE) INCYTE PHARM INC.
XX
PI Au-Young J, Coleman R, Hillman JL;
XX
DR WPI; 1998-110529/10.
XX
DR N-PSDB; AAV09218.
XX
PT New human monocyte chemotactic proprotein - has homology to CC

Amino acid sequenc
Protein of WT-MCP-
MCP-2 chemokine pr
Human chemokine hM
Human monocyte che
Chemokine hMCP2.
Truncated monocyte
MCP. Synthetic.
Human monocyte che
Chemottractant pr
Macrophage chemot
Human prostate can
Monocyte chemotact
Human chemokine MC
Human monocyte che
Human MCP1 fragmen
HIV.Nef1 fusion pr
Human small induci
Human monocyte che
Human MCP precursor
Mouse/human hybrid
Chimeric chemokine
Chemottractant MC
Cytokine encoded b
Full-length polype
Small inducible cy
HIV.Nef1 fusion pr
Human polypeptide
Mouse/human hybrid
Chimeric chemokine
Human MCP3 fragmen
Human eosinocyte C
Human chemokine eo

PT chemokine(s) useful for identifying agent for treating auto-immune
 PT diseases or allergic responses

PS Claim 1; Pages 38-39; 53pp; English.

XX The is a human monocyte chemotactic protein sequence. Its cDNA was
 CC first identified in incyte clone 965517 from a breast cDNA library.
 CC Antisense nucleotides can be used to control human MCP expression
 CC especially where it may lead to inappropriate monocyte or macrophage
 CC activity causing damage associated with allergic responses to organs
 CC such as the lungs. Antisense nucleotides and MCP cDNA may be used
 CC in diagnostic assays of body fluids or biopsied tissues to detect
 CC expression levels of MCP. MCP cDNA may also be useful for
 CC treatment of disorders such as asthma, rheumatoid arthritis, NIDDM
 CC or cancer of the breast or bladder. Human MCP protein can be used to
 CC identify agonists, antagonists or inhibitors to modulate the activity of
 CC MCP in allergic responses or autoimmune diseases such as AIDS.

SQ Sequence 109 AA:

Query Match 100.0%; Score 567; DB 19; Length 109;
 Best Local Similarity 100.0%; Pred. No. 2.5e-59;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKLTPLPKMKVSAALCLLLMAATFSPGGLAOPDSVSIPTCCFNVINKRPIORLES 60
 DB 1 MKLTPLPKMKVSAALCLLLMAATFSPGGLAOPDSVSIPTCCFNVINKRPIORLES 60

OY 61 YTRITNIOCPKEAVIFKTRKGEVCADPKERWVRDSMKHLDQIFONLKP 109
 DB 61 YTRITNIOCPKEAVIFKTRKGEVCADPKERWVRDSMKHLDQIFONLKP 109

RESULT 2

ABG35167
 ID ABG35167 standard; Protein; 109 AA.

AC ABG35167;

DT 15-JUL-2002 (first entry)

XX Reference sequence for human SCYA8 polypeptide.

XX Human; single nucleotide polymorphism: SNP; monocyte chemotactic protein;
 KM small inducible cytokine subfamily A member 8; SCYA8; antiinflammatory;
 KM haplotyping; genotyping; inflammatory disease; HIV infection;
 KM human immunodeficiency virus; anti-HIV.

OS Homo sapiens.

XX WO200222888-A1.

XX 21-MAR-2002.

PF 17-SEP-2001; 2001WO-US29332.

XX 15-SEP-2000; 2000US-232755P.

XX (GENA-) GENAISSANCE PHARM INC.

PI Anastasio AE, Chew A, Han J, Lee HH;

DR WPI; 2002-371973/40.

XX N-PSDB; ABK70707.

PT New genetic variants of Small Inducible Cytokine subfamily A (Cys-Cys),
 PT Member 8 (monocyte Chemotactic protein) isogenes, useful for improving
 PT efficiency and reliability in drug development for treating diseases

PS Claim 29; Fig 3; 84pp; English.

CC The present invention relates to novel single nucleotide polymorphisms
 CC (SNPs) in the human small inducible cytokine subfamily A (Cys-Cys),

CC member 8 (monocyte chemotactic protein) (SCYA8) gene located on
 CC chromosome 17, and methods for haplotyping and/or genotyping the SCYA8
 CC gene. The methods of the invention make use of allele-specific
 CC oligonucleotides (ASOs) as probes and primers and/or primer-extension
 CC oligonucleotides for detecting the SCYA8 gene polymorphisms. The
 CC polynucleotides and screened compounds are useful for the treatment of
 CC diseases associated with SCYA8 activity, such as inflammatory diseases
 CC and human immunodeficiency virus (HIV) infection. The present sequence
 CC represents a reference sequence for the human SCYA8 polypeptide.

SQ Sequence 109 AA:

Query Match 100.0%; Score 567; DB 23; Length 109;
 Best Local Similarity 100.0%; Pred. No. 2.5e-59;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKLTPLPKMKVSAALCLLLMAATFSPGGLAOPDSVSIPTCCFNVINKRPIORLES 60
 DB 1 MKLTPLPKMKVSAALCLLLMAATFSPGGLAOPDSVSIPTCCFNVINKRPIORLES 60

OY 61 YTRITNIOCPKEAVIFKTRKGEVCADPKERWVRDSMKHLDQIFONLKP 109
 DB 61 YTRITNIOCPKEAVIFKTRKGEVCADPKERWVRDSMKHLDQIFONLKP 109

RESULT 3

AAW26655
 ID AAW26655 standard; Protein; 109 AA.

AC AAW26655;

DT 16-FEB-1998 (first entry)

XX Human beta-chemokine H1305 (MCP-2).

XX H1305; MCP-2; chemokine; human; chemottractant; chemotaxis;

XX virus infection; HIV; therapy; wound healing; tumour; antibody.

OS Homo sapiens.

XX WO9725427-A1.

XX 17-JUL-1997.

PF 10-JAN-1997; 97WO-US00379.

XX 12-JAN-1996; 96US-0586395.

XX (GENY) GENETICS INST INC.

PI Lavallie ER, McCoy JM, Racie LA;

DR WPI; 1997-372866/34.

XX N-PSDB; AAT91023.

PT New human beta-chemokine, H1305 and corresponding DNA - used in the
 PT treatment of viral infection, e.g. HIV, and in wound healing

PS Claim 1; Page 12-13; 21pp; English.

CC This protein comprises human beta-chemokine H1305, also known as
 CC MCP-2. Its sequence was deduced from a claimed cDNA clone (see
 CC AAT91023) isolated from a human peripheral blood mononuclear cell
 CC cDNA library. Also claimed are: (1) a host cell, preferably linked
 CC to a mammalian, transformed with a H1306 polynucleotide operably linked
 CC to an expression control sequence; (2) a recombinantly produced
 CC H1305 protein; and (3) a composition comprising an antibody which
 CC specifically reacts with the H1305 protein. The H1305 protein
 CC may be used in a composition for the treatment of a mammalian
 CC subject (claimed). It is thought to have chemokine activities and
 CC may therefore have an effect on chemotaxis or migration of blood
 CC cells. It may be useful for inhibiting viral replication,
 CC including replication of HIV, and may also be used for treatment of

CC wounds and to raise monoclonal and polyclonal antibodies which
 CC specifically react with H1305. Such antibodies may be used for
 CC therapy of certain tumours as they are capable of blocking the
 CC ligand binding of the H1305 protein or may promote clearance of
 CC the protein from the patient.

XX Sequence 109 AA;

Query Match 99.3%; Score 563; DB 18; Length 109;
 Best Local Similarity 99.1%; Pred. No. 7,4e-59;
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLTPLPSKMKVSAALCLLLMAATFSPGGLAOPDSVSIPITCCFNVINRKIPQRLS 60
 DB 1 MKLTPLPSKMKVSAALCLLLMAATFSPGGLAOPDSVSIPITCCFNVINRKIPQRLS 60

QY 61 YTRITNIQCPEKAVIFKTRGKEVCADPKERWRDMSKHLDOIFONLKP 109
 DB 61 YTRITNIQCPEKAVIFKTRGKEVCADPKERWRDMSKHLDOIFONLKP 109

RESULT 4

ABG35168
 ID ABG35168 standard; Protein; 109 AA.

XX AC ABG35168;

DT 15-JUL-2002 (first entry)

DE Polymorphic variant #1 of human SCYA8 polypeptide.

XX Human; single nucleotide polymorphism; SNP; monocyte chemotactic protein;
 KW small inducible cytokine subfamily A member 8; SCYA8; antiinflammatory;
 KW haplotyping; genotyping; inflammatory disease; HIV infection;
 KW human immunodeficiency virus; anti-HIV.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 79 /note= "Substitution of Lys to Gln"

XX WO200222888-A1.

XX PD 21-MAR-2002.

XX PF 17-SEP-2001; 2001WO-US29332.

XX PR 15-SEP-2000; 2000US-232755P.

XX PA (GENA-) GENAISSANCE PHARM INC.

XX PI Anastasio AE, Chew A, Han J, Lee HH;

XX DR WPI; 2002-371973/40.

XX PT New genetic variants of Small Inducible Cytokine Subfamily A (Cys-Cys),
 PT Member 8 (Monocyte Chemotactic protein) isogenes, useful for improving
 PT efficiency and reliability in drug development for treating diseases
 XX Claim 29; Page -: 84pp; English.

XX The present invention relates to novel single nucleotide polymorphisms
 CC (SNPs) in the human small inducible cytokine subfamily A (Cys-Cys),
 CC member 8 (monocyte chemotactic protein) (SCYA8) gene located on
 CC chromosome 17, and methods for haplotyping and/or genotyping the SCYA8
 CC gene. The methods of the invention make use of allele-specific
 CC oligonucleotides (ASOs) as probes and primers and/or primer-extension
 CC oligonucleotides for detecting the SCYA8 gene polymorphisms. The
 CC polymorphisms and screened compounds are useful for the treatment of
 CC diseases associated with SCYA8 activity, such as inflammatory diseases
 CC and human immunodeficiency virus (HIV) infection. The present sequence
 CC represents a polymorphic variant of the human SCYA8 polypeptide

CC (ABG35167).
 CC Note: The present sequence is not given in the specification but is
 CC created by the indexer from the information given in fig. 3 of the
 CC patent.

XX Sequence 109 AA;

Query Match 99.3%; Score 563; DB 23; Length 109;
 Best Local Similarity 99.1%; Pred. No. 7,4e-59;
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLTPLPSKMKVSAALCLLLMAATFSPGGLAOPDSVSIPITCCFNVINRKIPQRLS 60
 DB 1 MKLTPLPSKMKVSAALCLLLMAATFSPGGLAOPDSVSIPITCCFNVINRKIPQRLS 60

QY 61 YTRITNIQCPEKAVIFKTRGKEVCADPKERWRDMSKHLDOIFONLKP 109
 DB 61 YTRITNIQCPEKAVIFKTRGKEVCADPKERWRDMSKHLDOIFONLKP 109

RESULT 5

ABG35169
 ID ABG35169 standard; Protein; 109 AA.

XX AC ABG35169;

DT 15-JUL-2002 (first entry)

DE Polymorphic variant #2 of human SCYA8 polypeptide.

XX Human; single nucleotide polymorphism; SNP; monocyte chemotactic protein;
 KW small inducible cytokine subfamily A member 8; SCYA8; antiinflammatory;
 KW haplotyping; genotyping; inflammatory disease; HIV infection;
 KW human immunodeficiency virus; anti-HIV.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 84 /note= "Substitution of Val to Phe"

XX WO200222888-A1.

XX PD 21-MAR-2002.

XX PF 17-SEP-2001; 2001WO-US29332.

XX PR 15-SEP-2000; 2000US-232755P.

XX PA (GENA-) GENAISSANCE PHARM INC.

XX PI Anastasio AE, Chew A, Han J, Lee HH;

XX DR WPI; 2002-371973/40.

XX PT New genetic variants of Small Inducible Cytokine Subfamily A (Cys-Cys),
 PT Member 8 (Monocyte Chemotactic protein) isogenes, useful for improving
 PT efficiency and reliability in drug development for treating diseases
 XX Claim 29; Page -: 84pp; English.

XX The present invention relates to novel single nucleotide polymorphisms
 CC (SNPs) in the human small inducible cytokine subfamily A (Cys-Cys),
 CC member 8 (monocyte chemotactic protein) (SCYA8) gene located on
 CC chromosome 17, and methods for haplotyping and/or genotyping the SCYA8
 CC gene. The methods of the invention make use of allele-specific
 CC oligonucleotides (ASOs) as probes and primers and/or primer-extension
 CC oligonucleotides for detecting the SCYA8 gene polymorphisms. The
 CC polymorphisms and screened compounds are useful for the treatment of
 CC diseases associated with SCYA8 activity, such as inflammatory diseases
 CC and human immunodeficiency virus (HIV) infection. The present sequence
 CC represents a polymorphic variant of the human SCYA8 polypeptide
 CC (ABG35167).

CC Note: The present sequence is not given in the specification but is
CC created by the indexer from the information given in fig. 3 of the
CC patent.

XX Sequence 109 AA:

Query Match 99.1%; Score 562; DB 23; Length 109;
Best Local Similarity 99.1%; Pred. No. 9.7e-59;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLTPSPSKKYSALLCLLIMATPSPOGLAOPDSVSIPTCCFVYINRKIPRIQRLES 60
DB 1 MKLTPSPSKKYSALLCLLIMATPSPOGLAOPDSVSIPTCCFVYINRKIPRIQRLES 60

OY 61 YTRITNOCCKEAVIEFTKRGKVCADPKERWVDSMKHLDQIFONLKP 109
DB 61 YTRITNOCCKEAVIEFTKRGKVCADPKERWVDSMKHLDQIFONLKP 109

RESULT 6
AA05300

ID AAY05300 standard; protein; 99 AA.

AC AAY05300;

DT 25-JUN-1999 (first entry)

DE C-C chemokine, MCP2.

XX C-C chemokine; RANTES; MCP2; chemokine antagonist; inflammatory disease;

KW HIV infection; tumour; angiogenesis-related disease; autoimmune disease;

KW haematopoiesis-related disease; CD26/DPP IV; immune disease; diagnosis;

KW atherosclerosis; pulmonary disease; skin disorder; therapy.

OS Homo sapiens.

XX EP905240-A1.

XX 31-MAR-1999.

PF 19-DEC-1997; 97EP-0122471.

PR 29-SEP-1997; 97EP-0116863.

XX (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.

PI Proost P, Struyf S, Van Damme J;

DR WPI; 1999-216695/19.

XX New amino-terminally truncated C-C chemokines have antagonistic

PT activity, for treatment of immune, inflammatory and infectious

PT diseases

XX Claim 4: Fig 1: 30pp; English.

PS This sequence represents the C-C chemokine MCP2. The invention relates

CC to amino-terminally truncated C-C chemokines, having chemokine

CC antagonistic activity. The truncated chemokines are specifically

CC residues 26 to 91 of the RANTES sequence (see AAY05299) or residues 29 to

CC 99 of the MCP2 sequence (this sequence). The new chemokines are useful

CC as medicaments, for diagnosis and/or treatment of diseases which require

CC antagonistic activity of a chemokine e.g. inflammatory diseases, HIV

CC infection, tumours, and angiogenesis- and haematopoiesis-related

CC diseases. The invention also relates to the use of CD26/DPP IV for

CC treatment of inflammatory, immune and infectious diseases, including

CC autoimmune diseases, atherosclerosis, pulmonary diseases and skin

CC disorders.

XX Sequence 99 AA;

SQ Query Match 91.2%; Score 517; DB 20; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.9e-53;

Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 MKVSAALLCLLIMATPSPOGLAOPDSVSIPTCCFVYINRKIPRIQRLESYTRITNIOCP 70
DB 1 MKVSAALLCLLIMATPSPOGLAOPDSVSIPTCCFVYINRKIPRIQRLESYTRITNIOCP 60

OY 71 KEAVIFKTRGKVCADPKERWVDSMKHLDQIFONLKP 109
DB 61 KEAVIFKTRGKVCADPKERWVDSMKHLDQIFONLKP 99

RESULT 7
AA07233
ID AAY07233 standard; protein; 99 AA.

AC AAY07233;

DT 06-JUL-1999 (first entry)

DE Wild type monocyte chemotactic protein 2.

XX Wild type; C-C chemokine; monocyte chemotactic protein 2; MCP2; HIV;

KW regulated on activation normal T-cell expressed and secreted; RANTES;

KW truncation; antagonist; medicaments; diagnosis; inflammation; infection;

KW tumour; angiogenesis; hematopoiesis; autoimmune disease; atherosclerosis;

KW pulmonary disease; skin disorder.

XX Homo sapiens.

XX EP906954-A1.

XX 07-APR-1999.

PF 29-SEP-1997; 97EP-0116863.

PR 29-SEP-1997; 97EP-0116863.

XX (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.

PI Proost P, Struyf S, Van Damme J;

DR WPI; 1999-207108/18.

XX New amino-terminally truncated C-C chemokines have antagonistic

PT activity for treatment of immune, inflammatory and infectious

PT diseases

XX Disclosure; Fig 1: 29pp; English.

PS This sequence represents the wild type C-C chemokine monocyte chemotactic

CC protein 2 (MCP2). The invention relates the generation of amino-terminal

CC truncated C-C chemokines, having chemokine antagonistic activity. The

CC new chemokines are useful as medicaments, for diagnosis and/or treatment

CC of diseases which require antagonistic activity of a chemokine e.g.

CC inflammatory diseases, HIV infection, tumours, and angiogenesis- and

CC hematopoiesis-related diseases, including auto-immune diseases,

CC atherosclerosis, pulmonary diseases and skin disorders.

XX Sequence 99 AA;

SQ Query Match 91.2%; Score 517; DB 20; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.9e-53;

Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 MKVSAALLCLLIMATPSPOGLAOPDSVSIPTCCFVYINRKIPRIQRLESYTRITNIOCP 70
DB 1 MKVSAALLCLLIMATPSPOGLAOPDSVSIPTCCFVYINRKIPRIQRLESYTRITNIOCP 60

OY 71 KEAVIFKTRGKVCADPKERWVDSMKHLDQIFONLKP 109
DB 61 KEAVIFKTRGKVCADPKERWVDSMKHLDQIFONLKP 99

ID	AA	Query Match	Best Local Similarity	Matches	99	Conservative	91.2%	Score	517	DB	20	Length	99	Pred. No.	1.9e-53	Indels	0	Gaps	0
RESULT 8	AAV07237	standard; protein; 99 AA.																	
XX	AAV07237																		
AC	AAV07237																		
DT	06-JUL-1999	(first entry)																	
XX																			
DE	Wild type monocyte chemotactic protein 2.																		
XX																			
KW	Wild type; C-C chemokine; monocyte chemotactic protein 2; MCP2; HIV;																		
KW	regulated on activation normal T-cell expressed and secreted; RANTES;																		
KW	truncated; antagonist; medicaments; diagnosis; inflammation; infection;																		
KW	tumour; angiogenesis; hematopoiesis; autoimmune disease; atherosclerosis;																		
KW	pulmonary disease; skin disorder.																		
XX																			
OS	Homo sapiens.																		
XX																			
PN	EP905241-A1.																		
XX																			
PD	31-MAR-1999.																		
XX																			
PE	10-MAR-1998; 98EP-0104216.																		
XX																			
PR	19-DEC-1997; 97EP-0122471.																		
XX																			
PR	29-SEP-1997; 97EP-0116863.																		
XX																			
PA	(ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.																		
PI	Proost P, Struyf S, Van Damme J;																		
XX																			
DR	WPI; 1999-206774/18.																		
XX																			
PT	New amino-terminally truncated C-C chemokines have antagonistic																		
PT	activity for treatment of immune, inflammatory and infectious																		
XX	diseases																		
PS	Disclosure: Fig 1; 36pp: English.																		
XX																			
CC	This sequence represents the wild type C-C chemokine monocyte chemotactic																		
CC	protein 2 (MCP2). The invention relates the generation of amino-terminal																		
CC	truncated C-C chemokines, having chemokine antagonistic activity. The																		
CC	new chemokines are useful as medicaments, for diagnosis and/or treatment																		
CC	of diseases which require antagonistic activity of a chemokine e.g.																		

KM		Macrophage recruitment; chemokine derivative; MCP-1; osteoporosis;
KM		monocyte chemoattractant protein-1; inflammation; atherosclerosis; HIV;
KX		AIDS; stroke; psoriasis; autoimmune disease; hypertension; endotoxaemia;
KM		basophil-mediated disease; myocardial infarction; acute ischaemia;
KW		rheumatoid arthritis; contraception.
XX		
OS	Homo sapiens.	
XX		
PH		Location/Qualifiers
FT	Key	Misc-difference 47 /note= "encoded by CAA"
XX		
PN	WO20042071-A2.	
PD	20-Jul-2000.	
XX		
PF	12-JAN-2000; 2000WO-US00821.	
XX		
PR	12-JAN-1999; 99US-0229071.	
PR	17-MAR-1999; 99US-0271192.	
PR	01-DEC-1999; 99US-0452406.	
PA	(NEOR-) NEORX CORP.	
XX		
PI	Gralinger DJ, Tatalick LM;	
DR	WPI: 2000-499101/44. N-PSTDB: AAA74886.	
XX		
PT	New peptide 3, amide and heterocyclic compounds and saccharide conjugates used for inhibiting chemokine induced activity and for treating e.g. stroke, vascular diseases, autoimmune diseases and tumour growth _	
PS	Example 1; Page 134; 387pp; English.	
XX		
CC	The present invention concerns the identification of a number of chemokines which can be used to produce derivatives, agonists and antagonists which are then useful in disease treatment. The chemokines include sequences AAB15785-B15794, AAB15803-B15813 and AAB15831-B15848. These chemokine derivatives can be used to treat diseases such as AIDS, psoriasis, inflammatory diseases, osteoporosis, HIV infection and rheumatoid arthritis, and can be used to prevent strokes and as contraceptives. The coding sequences for the chemokines can be used in gene therapy for the same diseases, as well as in the production of animal models.	
SO	Sequence 77 AA:	
Query Match	72.7%; Score 412; DB 21; Length 77;	
Best Local Similarity	100.0%; Pred. No. 3.8e-41;	
Matches 77; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
OY	33 AQPDSVSPITPCFNVNRKIPIDLESTRITNIQCCKEAVIFTKRGKEVCAPPKRM 92	
Db	1 AQPDSVSIPITPCFNVNRKIPIDLESTRITNIQCCKEAVIFTKRGKEVCAPPKRM 60	
OY	93 VRDSMKHLDQIFONLKP 109	
Db	61 VRDSMKHLDQIFONLKP 77	
RESULT 10		
ABB80903		
ID	ABB80903 standard; Protein: 77 AA.	
XX		
AC	ABB80903;	
DT	08-Oct-2002 (first entry)	
DE	Human MCP2 fragment.	

XX Eotaxin: eosinophil; chemotaxis; cytostatic; antiinflammatory; cartant;
 KW antiallergic; immunosuppressive; antiasthmatic; antiparasitic; histamine;
 KW dermatological; vasotropic; monocyte chemoattractive protein; MCP;
 KW gene therapy; antianaphylactic.
 XX
 OS Homo sapiens.
 XX
 PN US6403782-B1.
 XX
 PD 11-JUN-2002.
 XX
 PF 04-AUG-1999; 99US-0366887.
 XX
 PR 22-JUN-1995; 95US-000449P.
 PR 01-SEP-1995; 95US-0522713.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX (GEHO) GEN HOSPITAL CORP.
 PI Luster AD, Leder P, Rothenberg M, Garcia E;
 XX
 DR WPI: 2002-565447/60.
 XX
 PT New DNA encoding murine, guinea pig or human eotaxin polypeptides,
 PT useful for treating inflammation and tumorigenesis and in anticancer
 PT gene therapy
 XX
 PS Disclosure: Fig 3B; 42pp; English.
 XX
 CC The invention relates to polynucleotides encoding murine, guinea pig or
 CC human eotaxin polypeptides. The eotaxin polynucleotides are useful for
 CC modulating eosinophil chemotaxis, for increasing eosinophil chemotactic
 CC events, and for improving prognosis with tumours in patients. They are
 CC also useful for treating inflammation and tumorigenesis, and for
 CC reducing inflammation and cytotoxic damage caused by eosinophils, for
 CC e.g. during asthmatic reactions, eosinophilic pneumonia and allergic
 CC diseases, inflammatory bowel diseases, atopic dermatitis, urticaria,
 CC vasculitis, parasitic infections and eosinophil cardiac diseases. The
 CC eotaxin polynucleotides are also useful for modulating histamine release
 CC by modulating eotaxin activity or expression during anaphylaxis,
 CC urticaria and allergic reactions. They are useful for detecting and
 CC monitoring eosinophil mediating conditions, and in anti-cancer gene
 CC therapy. The present sequence represents a human monocyte chemoattractive
 CC protein (MCP)2 fragment.
 CC
 XX
 SO Sequence 77 AA:
 Query Match 72.7%; Score 412; DB 23; Length 77;
 Best Local Similarity 100.0%; Pred. No. 3.8e-41;
 Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 33 AOPDSVSIPTCCFNVINRKIPQRLSESYRTINIOCPKRAVIFKTRGKEVCADPKRRW 92
 DB 1 AOPDSVSIPTCCFNVINRKIPQRLSESYRTINIOCPKRAVIFKTRGKEVCADPKRRW 60
 QY 93 VRDSMKHLDQIFQNLKP 109
 DB 61 VRDSMKHLDQIFQNLKP 77

RESULT 11

AAV69031
 ID AAV69031 standard; protein: 76 AA.
 XX
 AC AAV69031;
 XX
 DT 30-MAY-2000 (first entry)
 XX
 DE Amino acid sequence of chemokine receptor ligand MCP-2.
 KW Chemokine receptor; ligand; inflammatory response; immune effector cell;
 KW secondary tissue damage; central nervous system injury; MCP-2;

KW CNS inflammatory disease; neurodegenerative disorder; heart disease;
 KW inflammatory eye disease; inflammatory bowel disease;
 KW inflammatory joint disease; inflammatory kidney; renal disease;
 KW inflammatory lung disease; inflammatory nasal disease;
 KW inflammatory thyroid disease; thyroiditis; cytokine-regulated cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200004926-A2.
 XX
 PD 03-FEB-2000.
 XX
 PF 21-JUL-1999; 99WO-CA00659.
 XX
 PR 22-JUL-1998; 98US-0120523.
 XX
 PA (OSPR-) OSPREY PHARM LTD.
 XX
 PI McDonald JR, Coggins PJ;
 XX
 DR WPI: 2000-182542/16.
 XX
 PT A new therapeutic agent comprising a conjugate for treating secondary
 PT tissue damage and other disease conditions like Alzheimer's disease,
 PT stroke, Parkinson's disease and atherosclerosis
 XX
 PS Disclosure: Page 60; 204pp; English.
 XX
 CC The present sequence represents a chemokine receptor ligand. The present
 CC ligand can be incorporated into the conjugates of the invention. The
 CC specification describes a conjugate, comprising a targeted agent and a
 CC chemokine receptor ligand. The conjugate binds to a chemokine receptor
 CC resulting in internalisation of the targeted agent in cells bearing the
 CC receptor. The conjugates are used for formulating a medicament or for
 CC treating disorders associated with inflammatory responses resulting from
 CC activation, proliferation and migration of immune effector cells. The
 CC disorders or disease states comprise secondary tissue damage such as
 CC central nervous system (CNS) injury, CNS inflammatory diseases,
 CC neurodegenerative disorders, heart disease, inflammatory eye diseases,
 CC inflammatory bowel diseases, inflammatory joint diseases, inflammatory
 CC kidney or renal diseases, inflammatory lung diseases, inflammatory
 CC nasal diseases, inflammatory thyroid disease such as thyroiditis, or
 CC cytokine-regulated cancers.
 CC
 XX
 SO Sequence 76 AA:
 Query Match 72.0%; Score 408; DB 21; Length 76;
 Best Local Similarity 100.0%; Pred. No. 1.1e-40;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 34 OPDSVSIPTCCFNVINRKIPQRLSESYRTINIOCPKRAVIFKTRGKEVCADPKRRW 93
 DB 1 OPDSVSIPTCCFNVINRKIPQRLSESYRTINIOCPKRAVIFKTRGKEVCADPKRRW 60
 QY 94 RDSMKHLDQIFQNLKP 109
 DB 61 RDSMKHLDQIFQNLKP 76

RESULT 12

AAO21099
 ID AAO21099 standard; protein: 76 AA.
 XX
 AC AAO21099;
 XX
 DT 19-JUL-2002 (first entry)
 XX
 DE Protein of WT-MCP-2.
 XX
 DE RANTES; neuroprotective; antiallergic; antiinflammatory; anti-HIV; human;
 KW chemokine mutant; cationic site; multiple sclerosis; HIV infection;
 KW inflammatory disease; demyelinating disease; allergic.

OS Homo sapiens.
XX WO200228419-A2.
PN
XX
PD 11-APR-2002.
XX
XX 03-OCT-2001; 2001WO-EP11428.
XX
XX 04-OCT-2000; 2000EP-0121665.
PR
XX
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
XX
PI Proudfoot A, Wells TNC, Kosco-Vilbois M;
XX
DR WPI; 2002-340073/37.
XX
PT A mutant of the human CC chemokine RANTES with two mutations in the
PT cationic site of the 40's loop is used for treatment of multiple
PT sclerosis and/or demyelinating diseases -
XX
XX Examples; Page 46; 46pp; English.
PS
XX The invention relates to a truncated and mutated human RANTES (a CC
CC chemokine mutant), comprising the amino sequence of 91 amino acids as
CC given in the specification. The CC chemokine mutant RANTES, with two
CC mutations in the cationic site is useful for the preparation of a
CC pharmaceutical composition used in treating multiple sclerosis or other
CC demyelinating diseases. The mutant with single mutations at cationic
CC sites is used for the treatment of HIV infection and/or other allergic or
CC inflammatory diseases. This sequence represents an example of a wild-type
CC chemokine protein used in the invention.
SQ Sequence 76 AA;

Query Match 72.0%; Score 408; DB 23; Length 76;
Best Local Similarity 100.0%; Pred. No. 1,1e-40;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 34 QPDSVSIPTCCFNVNINRKIPRIORLESYTRITNIQCPKEAVIFKTRKGEVCADPKERWV 93
DB 1 QPDSVSIPTCCFNVNINRKIPRIORLESYTRITNIQCPKEAVIFKTRKGEVCADPKERWV 60

OY 94 RDSMKHLDQIFONLKP 109
DB 61 RDSMKHLDQIFONLKP 76

RESULT 13

AAO21109
ID AAO21109 standard; Protein; 76 AA.

AC AAO21109;

DT 19-JUL-2002 (first entry)

DE MCP-2 chemokine protein containing 40's loop and cationic site.

XX RANTES; neuroprotective; anti-allergic; anti-inflammatory; anti-HIV; human;
KW chemokine mutant; cationic site; multiple sclerosis; HIV infection;
KW inflammatory disease; demyelinating disease; allergic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Region 36..52
FT /label= 40's_loop

FT Misc-difference 46..49
FT /label= Cationic_site

XX WO200228419-A2.

XX 11-APR-2002.

XX

PE 03-OCT-2001; 2001WO-EP11428.
XX
XX 04-OCT-2000; 2000EP-0121665.
PR
XX
XX (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
PA
XX
XX Proudfoot A, Wells TNC, Kosco-Vilbois M;
PI
XX
XX WPI; 2002-340073/37.
DR
XX
PT A mutant of the human CC chemokine RANTES with two mutations in the
PT cationic site of the 40's loop is used for treatment of multiple
PT sclerosis and/or demyelinating diseases -
XX
XX Disclosure; Fig 1; 46pp; English.
PS
XX The invention relates to a truncated and mutated human RANTES (a CC
CC chemokine mutant), comprising the amino sequence of 91 amino acids as
CC given in the specification. The CC chemokine mutant RANTES, with two
CC mutations in the cationic site is useful for the preparation of a
CC pharmaceutical composition used in treating multiple sclerosis or other
CC demyelinating diseases. The mutant with single mutations at cationic
CC sites is used for the treatment of HIV infection and/or other allergic or
CC inflammatory diseases. This sequence represents an example of a CC
CC chemokine protein containing a 40's loop and cationic site of the
CC invention.
SQ Sequence 76 AA;

Query Match 72.0%; Score 408; DB 23; Length 76;
Best Local Similarity 100.0%; Pred. No. 1,1e-40;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 34 QPDSVSIPTCCFNVNINRKIPRIORLESYTRITNIQCPKEAVIFKTRKGEVCADPKERWV 93
DB 1 QPDSVSIPTCCFNVNINRKIPRIORLESYTRITNIQCPKEAVIFKTRKGEVCADPKERWV 60

OY 94 RDSMKHLDQIFONLKP 109
DB 61 RDSMKHLDQIFONLKP 76

RESULT 14

AAQ78390
ID AAQ78390 standard; protein; 76 AA.

AC AAQ78390;

DT 30-MAY-2002 (first entry)

DE Human chemokine hMCP-2.

XX Antigen presenting cell; APC; chemotaxin; immune response; antigen;

XX chemokine; antitumor; cytostatic; antimicrobial; toxin;

XX pathogenic agent; cancer; melanoma; thyroid carcinoma;

XX renal cell carcinoma; tumor-associated antigen; human; hMCP-2.

OS Homo sapiens.

XX WO200180882-A2.

XX 01-NOV-2001.

XX 20-APR-2001; 2001WO-US12950.

XX 21-APR-2000; 2000US-198839P.

XX 12-APR-2001; 2001US-0834814.

XX (CHEM-) CHEMOCENTRIX INC.

XX Schall TJ, Talbot D;

XX WPI; 2002-034405/04.

XX

XX Use of a composition containing an antigen presenting cell-chemotaxin
PT which is a chemokine polypeptide or its variant or a polynucleotide
PT encoding the protein, for inducing immune response to an antigen in a
PT subject
XX
PS Claim 7; Fig 2; 60pp; English.
XX
CC The present sequence is that of a human chemokine polypeptide designated
CC hMCP-2, used in the compositions of the invention. The specification
CC describes the use of a composition containing an antigen presenting cell
CC (APC)-chemotaxin for inducing an immune response to an antigen in a
CC subject, in the manufacture of a medicament, where the APC-chemotaxin is
CC a chemokine polypeptide or its variant, or a polynucleotide encoding the
CC chemokine polypeptide or its variant. The invention has antitumor,
CC cytostatic and antimicrobial activity. The compositions of the invention
CC can contain one or more antigens (or antigen containing polynucleotides)
CC and may be administered in the same mixture as the APC-chemotaxin or
CC separately. Synthetic (mimetic) or naturally occurring chemokines may be
CC used. The polypeptides of the invention are used to induce an immune
CC response by recruiting APCs to areas of antigen contact. The compositions
CC of the invention are useful for providing protection from foreign
CC infectious pathogenic agents (bacteria, virus, etc.,) prior to expected
CC or possible exposure; for treating cancers, melanomas,
CC thyroid carcinomas, lung and breast cancers, renal cell carcinomas etc.,
CC here the antigen present in the composition is a tumour-associated
CC antigen. The use of APC-chemotaxins provides an accelerated immune
CC response in a host following administration of antigen, a more effective
CC response to administration of, or exposure to, very small quantities of
CC an antigen (e.g., toxin or pathogen) due to increased antigen uptake by
CC APCs, and more effective anti-tumour therapies.
XX
SQ Sequence 76 AA:
XX
Query Match 71.3%; Score 404; DB 23; Length 76;
Best Local Similarity 98.7%; Pred. No. 3.3e-40;
Matches 75; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 34 QPDSVSIPTCCFNVIKRIPIORLESYTRITNIQCPKEAVIFKTRGKEVCADPKRRWV 93
DB 1 QPDSVSIPTCCFNVIKRIPIORLESYTRITNIQCPKEAVIFKTRGKEVCADPKRRWV 60
QY 94 RDSMKHLDOIIFONLKP 109
DB 61 RDSMKHLDOIIFONLKP 76
XX
RESULT 15
AAG68353
ID AAG68353 standard; peptide; 76 AA.
XX
AC AAG68353;
XX
DT 01-MAR-2002 (first entry)
XX
DE Human monocyte chemotactic protein 2 (MCP2) amino acid sequence.
XX
KW Human; mouse; monocyte chemotactic protein 2; hMCP2; MCP2; mC10; mMDC;
KW chimeric chemokine; immune response; cytostatic; antimicrobial;
KW immunostimulant; vaccine; cancer; breast cancer; lung cancer;
KW carcinoma; melanoma; tumour; hybridline.
XX
OS Homo sapiens.
XX
PN MO200180887-A2.
XX
PD 01-NOV-2001.
XX
PF 12-APR-2001; 2001WO-US12162.
XX
PR 21-APR-2000; 2000US-198839P.
XX
PA (CHEM-) CHEMOCENTRIX INC.

XX
PI Schall TJ, Talbot D;
XX
DR WPI: 2002-049246/06.
XX
XX Inducing an immune response to an antigen to confer non-specific
PT protection while the body is generating the adaptive response,
PT comprises administering a composition containing an antigen-presenting
PT cell chemotaxin
XX
PS Example 5; Fig 2; 60pp; English.
XX
XX The present invention describes a method for inducing an immune response
CC to an antigen in a subject. The method comprises administering a
CC composition containing an antigen-presenting cell chemotaxin
CC (APC-chemotaxin), where the APC-chemotaxin is a chemokine polypeptide,
CC its variant, or a polynucleotide encoding the chemokine polypeptide or
CC its variant. The APC-chemotaxin has cytostatic, antimicrobial and
CC immunostimulant activities, and can be used in vaccine production.
CC The method can be used for inducing or enhancing an immune response,
CC or for providing protection from exogenous foreign infectious pathogenic
CC agents prior to expected or possible exposure, or to individuals
CC displaying symptoms of exposure. The method may be used to treat cancers
CC e.g. breast cancer, lung cancer, carcinomas, melanomas, and tumours.
CC The present sequence represents a human monocyte chemotactic protein 2
CC (hMCP2) amino acid sequence, which is used in an example from the
CC present invention for the design of hybridlines (chimeric chemokines).
XX
SQ Sequence 76 AA:
XX
Query Match 71.3%; Score 404; DB 23; Length 76;
Best Local Similarity 98.7%; Pred. No. 3.3e-40;
Matches 75; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 34 QPDSVSIPTCCFNVIKRIPIORLESYTRITNIQCPKEAVIFKTRGKEVCADPKRRWV 93
DB 1 QPDSVSIPTCCFNVIKRIPIORLESYTRITNIQCPKEAVIFKTRGKEVCADPKRRWV 60
QY 94 RDSMKHLDOIIFONLKP 109
DB 61 RDSMKHLDOIIFONLKP 76
XX
Search completed: February 18, 2003, 03:02:52
Job time : 71 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2003, 03:03:01 ; Search time 19 Seconds
(without alignments)
146,570 Million cell updates/sec

Title: US-10-033-067-1

Perfect score: 567
Sequence: 1 MKLTPPLPSKMKVSALLCLL.....ERWVRDSMKHLIDIFQNLKP 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 140259 segs, 25548876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB pep: *
2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB pep: *
3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB pep: *
4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB pep: *
5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB pep: *
6: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB pep: *
7: /cgn2_6/ptodata/1/pubppa/PCTUS_PUBCOMB pep: *
8: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB pep: *
9: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB pep: *
10: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB pep: *
11: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB pep: *
12: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB pep: *
13: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB pep: *
14: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	567	100.0	109	US-10-033-067-1	Sequence 1, Appl
2	412	72.7	77	US-08-927-939-17	Sequence 17, Appl
3	412	72.7	77	US-10-057-275-10	Sequence 10, Appl
4	412	72.7	77	US-09-834-794A-24	Sequence 24, Appl
5	412	72.7	77	US-09-834-795A-24	Sequence 24, Appl
6	408	72.0	76	US-09-792-793A-21	Sequence 21, Appl
7	396	69.8	74	US-09-195-457-6	Sequence 6, Appl
8	375	66.1	97	US-10-057-275-5	Sequence 5, Appl
9	367	64.7	97	US-08-927-939-16	Sequence 16, Appl
10	367	64.7	99	US-10-057-275-9	Sequence 9, Appl
11	367	64.7	99	US-10-033-067-4	Sequence 4, Appl
12	367	64.7	99	US-10-141-965-5	Sequence 5, Appl
13	357	63.0	109	US-10-057-275-11	Sequence 11, Appl
14	357	63.0	109	US-10-033-067-3	Sequence 3, Appl
15	354	62.4	99	US-09-834-794A-28	Sequence 28, Appl
16	354	62.4	99	US-09-834-795A-28	Sequence 28, Appl
17	350	61.7	97	US-08-927-939-25	Sequence 25, Appl
18	350	61.7	97	US-10-114-893-52	Sequence 52, Appl
19	350	61.7	97	US-09-834-794A-26	Sequence 26, Appl

20	350	61.7	97	10	US-09-834-795A-26	Sequence 26, Appl
21	346	61.0	97	9	US-10-057-275-2	Sequence 2, Appl
22	337	59.4	99	8	US-08-927-939-18	Sequence 18, Appl
23	337	59.4	99	9	US-10-125-451-18	Sequence 18, Appl
24	332	58.6	99	9	US-09-834-794A-27	Sequence 27, Appl
25	332	58.6	99	10	US-09-834-795A-27	Sequence 27, Appl
26	328.5	57.9	98	8	US-08-927-939-50	Sequence 50, Appl
27	328.5	57.9	98	8	US-08-927-939-83	Sequence 83, Appl
28	328.5	57.9	98	9	US-10-164-621-4	Sequence 4, Appl
29	328.5	57.9	98	9	US-10-125-451-4	Sequence 4, Appl
30	328.5	57.9	98	9	US-09-834-794A-25	Sequence 25, Appl
31	328.5	57.9	98	10	US-09-834-795A-25	Sequence 25, Appl
32	328.5	57.9	98	10	US-09-872-611A-2	Sequence 2, Appl
33	268	47.3	76	9	US-09-792-793A-20	Sequence 20, Appl
34	268	47.3	76	10	US-09-195-457-5	Sequence 5, Appl
35	268	47.3	325	5	US-09-792-793A-72	Sequence 71, Appl
36	268	47.3	327	9	US-09-792-793A-71	Sequence 72, Appl
37	268	47.3	332	9	US-09-792-793A-73	Sequence 73, Appl
38	267	47.1	74	9	US-09-792-793A-13	Sequence 13, Appl
39	267	47.1	74	9	US-10-125-451-20	Sequence 20, Appl
40	267	47.1	323	9	US-09-792-793A-80	Sequence 80, Appl
41	267	47.1	325	9	US-09-792-793A-81	Sequence 81, Appl
42	267	47.1	330	9	US-09-792-793A-82	Sequence 82, Appl
43	259	45.7	148	8	US-08-927-939-26	Sequence 26, Appl
44	243	42.9	76	9	US-09-792-793A-22	Sequence 22, Appl
45	243	42.9	76	9	US-10-125-451-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-10-033-067-1
Sequence 1, Application US/10033067
Patent No. US20020164704A1
GENERAL INFORMATION:
APPLICANT: Coleman, Roger
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN MONOCYTE CHEMOTACTIC PROTEIN
FILE REFERENCE: PR-0069-1 CON
CURRENT APPLICATION NUMBER: US/10/033,067
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: 08/683,655
PRIOR FILING DATE: 1996-07-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PERL Program
SEQ ID NO 1
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc-feature
OTHER INFORMATION: Incyte ID NO. US20020164704A1 965517CD1
US-10-033-067-1

Query Match 100.0%; Score 567; DB 9; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.6e-53;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKLTPPLPSKMKVSALLCLLIMATFSPQGLAOPDSVSIPTCCFNVINRRIPIDRLS 60
DB 1 MKLTPPLPSKMKVSALLCLLIMATFSPQGLAOPDSVSIPTCCFNVINRRIPIDRLS 60
OY 61 YTRINNICPKKAVIFKTRKREKVCADPKERWVRDSMKHLIDIFQNLKP 109
DB 61 YTRINNICPKKAVIFKTRKREKVCADPKERWVRDSMKHLIDIFQNLKP 109

RESULT 2
US-08-927-939-17
Sequence 17, Application US/08927939
Patent No. US2001000640A1

```
; GENERAL INFORMATION:
; APPLICANT: Graininger, David J.
; APPLICANT: Tatalick, Lauren Marie
; TITLE OF INVENTION: Compounds and methods to inhibit or
; FILE REFERENCE: 295.022051
; CURRENT APPLICATION NUMBER: US/08/927,939
; CURRENT FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-927-939-17

Query Match      72.7%; Score 412; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 3.3e-37;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AOPDSVSIPTCCFNVNINRKIPQRLSEYTRITNIQCPKEAVIFKTKRGKVCADPKERW 92
    |||
Db 1 AOPDSVSIPTCCFNVNINRKIPQRLSEYTRITNIQCPKEAVIFKTKRGKVCADPKERW 60

QY 93 VRDSMKHLDQIFONLKP 109
    |||
Db 61 VRDSMKHLDQIFONLKP 77

RESULT 3
US-10-057-275-10
; Sequence 10, Application US/10057275
; Patent No. US20020155545A1
; GENERAL INFORMATION:
; APPLICANT: Coleman, Roger
; Bandman, Olga
; Wilde, Craig G.
; TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/057,275
; FILING DATE: 25-Jan-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/380,740A
; FILING DATE: February 17, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0027 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
```

```
; CLONE: MCP-2
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
; US-10-057-275-10

Query Match      72.7%; Score 412; DB 9; Length 77;
Best Local Similarity 100.0%; Pred. No. 3.3e-37;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AOPDSVSIPTCCFNVNINRKIPQRLSEYTRITNIQCPKEAVIFKTKRGKVCADPKERW 92
    |||
Db 1 AOPDSVSIPTCCFNVNINRKIPQRLSEYTRITNIQCPKEAVIFKTKRGKVCADPKERW 60

QY 93 VRDSMKHLDQIFONLKP 109
    |||
Db 61 VRDSMKHLDQIFONLKP 77

RESULT 4
US-09-834-794A-24
; Sequence 24, Application US/09834794A
; Publication No. US20030026777A1
; GENERAL INFORMATION:
; APPLICANT: Lawrence, Papsidero
; APPLICANT: Lyn, Dyster
; APPLICANT: Jana, Frustaci
; TITLE OF INVENTION: Detection and Treatment of Breast Cancer
; FILE REFERENCE: 3380/1127-US4
; CURRENT APPLICATION NUMBER: US/09/834,794A
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 09/146,580
; PRIOR FILING DATE: 1998-09-03
; PRIOR APPLICATION NUMBER: 60/071,899
; PRIOR FILING DATE: 1998-01-20
; PRIOR APPLICATION NUMBER: 60/092,155
; PRIOR FILING DATE: 1998-07-09
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-834-794A-24

Query Match      72.7%; Score 412; DB 9; Length 77;
Best Local Similarity 100.0%; Pred. No. 3.3e-37;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AOPDSVSIPTCCFNVNINRKIPQRLSEYTRITNIQCPKEAVIFKTKRGKVCADPKERW 92
    |||
Db 1 AOPDSVSIPTCCFNVNINRKIPQRLSEYTRITNIQCPKEAVIFKTKRGKVCADPKERW 60

QY 93 VRDSMKHLDQIFONLKP 109
    |||
Db 61 VRDSMKHLDQIFONLKP 77

RESULT 5
US-09-834-795A-24
; Sequence 24, Application US/09834795A
; Patent No. US20020076710A1
; GENERAL INFORMATION:
; APPLICANT: Lawrence, Papsidero
; APPLICANT: Lyn, Dyster
; APPLICANT: Jana, Frustaci
; TITLE OF INVENTION: Detection and Treatment of Breast Cancer
; FILE REFERENCE: 3380/1127-US3
; CURRENT APPLICATION NUMBER: US/09/834,795A
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 09/146,580
; PRIOR FILING DATE: 1998-09-03
; PRIOR APPLICATION NUMBER: 60/071,899
; PRIOR FILING DATE: 1998-01-20
; PRIOR APPLICATION NUMBER: 60/092,155
```



```

OY      11 MKVSALLCLILMATFSPGCLAPDSVSIPTCCFNINRKPIPIORLESYRITNIQCP 70
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 MKVSALLALLLILIAAFPGCLAPDGDVPTTCCFNINRKIPROLESYRITTSKCS 60
OY      71 KEAVIFKTRGKEVCADPERKVRWRDMSMKHLDFIQLNKP 109
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      61 KPAVIFKTRAKQVCADPERKRVQDSMKHLK--QTpkp 97

RESULT 9
US-08-927-939-16
Sequence 16, Application US/08927939
Patent No. US2001000640A1
GENERAL INFORMATION:
APPLICANT: Grainger, David J.
APPLICANT: Tatalick, Lauren Marie
TITLE OF INVENTION: Compounds and methods to inhibit or
TITLE OF INVENTION: augment an inflammatory response.
FILE REFERENCE: 295.022051
CURRENT APPLICATION NUMBER: US/08/927,939
CURRENT FILING DATE: 1997-09-11
NUMBER OF SEQ ID NOS: 83
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 16
LENGTH: 99
TYPE: PRT
ORGANISM: Homo sapiens
US-08-927-939-16

```

```

GENERAL INFORMATION:
APPLICANT: LI, HAODONG
RUBEN, STEVEN M
SUTTON, GRANGER G III
TITLE OF INVENTION: HUMAN CHEMOKINE PROTEIN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/141,965
FILING DATE: 10-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/453,416
FILING DATE: 03-DEC-1999
APPLICATION NUMBER: US 09/044,855
FILING DATE: 20-MAR-1998
APPLICATION NUMBER: US 08/479,126
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 08/424,425
FILING DATE: 21-APR-1995
APPLICATION NUMBER: PCT/US94/05384
FILING DATE: 16-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: STEEFE, ERIC K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488, 034000C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-141-965-5

Query Match 64.7%, Score 367, DB 9, Length 99;
Best Local Similarity 69.4%, Pred. No. 2.7e-32;
Matches 68; Conservative 14; Mismatches 16; Indels 0; Gaps 0.

QY 11 MKVSAALICLLMLATSPGGIQAQDSVSIPTCCFNINRKIPRIORLESRYTINIOCP 70
Db 1 MKVSAALICLLILATFTIPQGLQADDAINAPVTCYINFTNRKISVQRLASTIRITSSKCP 60

QY 71 KEAVIFKTRGKEVCADPKRKERVNRVSRSMKHLQDIFONLK 108
Db 61 KEAVIFKTVAKELCADPKRKQKWDQSMHLDKQGTPTK 98

RESULT 13
US-10-057-275-11
; Sequence 11, Application US/10057275
; Patent No. US20020155545A1
GENERAL INFORMATION:
APPLICANT: Coleman, Roger
Bandman, Olga
Wilde, Craig G.
TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:

```

```

ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/057.275
FILING DATE: 25-Jan-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/390,740A
FILING DATE: February 17, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0027 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0195
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: MCP-3
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-057-275-11

Query Match 63.0%; Score 357; DB 9; Length 109;
Best Local Similarity 63.9%; Pred. No. 3,5e-31;
Matches 69; Conservative 11; Mismatches 28; Indels 0; Gaps 0;

QY 1 MLKTLPLSKKVSALLCLLMAATFSPQGLAOPDSVSIPTCCFNINRKIPRIORLES 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MWKMPSPSSNNKASALLCLLTLTAAPSPQGLAOPVGINSTTCYRINKKIPRIORLES 60

QY 61 YTRITNIOCPKEAVYIFKTRGKEVCADPEKRWVRDMSKHLDOI FQNLK 108
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 YRRTTSSHCPRVAIVFKTKLDEKICADPTQKMYVDPMKHLDKKTYTPK 108

RESULT 14
US-10-033-067-3
Sequence 3, Application US/10033067
Patent No. US20020164704A1
GENERAL INFORMATION:
APPLICANT: Coleman, Roger
APPLICANT: Hillman, Jennifer L.
APPLICANT: Au-Young, Janice
TITLE OF INVENTION: NOVEL HUMAN MONOCYTE CHEMOTACTIC PROTEIN
FILE REFERENCE: PF-0069-1 CON
CURRENT APPLICATION NUMBER: US/10/033.067
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: 08/683,655
PRIOR FILING DATE: 1996-07-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PERL Program
SEQ ID NO 3
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature

```


OTHER INFORMATION: GenBank ID No. US20020164704A1 g288397
US-10-033-067-3

Query Match	63.0%;	Score 357;	DB 9;	Length 109;
Best Local Similarity	63.9%;	Pred. No. 3.5e-31;		
Matches 69;	Conservative 11;	Mismatches 28;	Indels 0;	Gaps 0;

OY 1 MLKLTPLPSMKVSAALICLLMAATFSPOGLAQPDSVIPITCCFNVINRKIPQRLLES 60
| | | | | : | : | : |
Db 1 MKKPMSPSNKKASAAIICLLTAAAFSPGQAQPGINTSTPCCYRFINKKIEPQLLES 60

```

QY      61 YTRITNIQCPEAVIFKTKGKEVCADPKERWVDSMKHLDDIFQNLK 108
      1 1 1 : : 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      61 YRRTTSHCPREAVIFKTKLDEKICADPTQKWQDFMKHLDKKTQTTPK 108

```

RESULT 15
US-09-834-794A-28
: Sequence 28, Application US/09834794A

```

; GENERAL INFORMATION:
; APPLICANT: Lawrence, Papsidero
; APPLICANT: LYD, Dyster

```

```

: TITLE OF INVENTION: Detection and Treatment of Breast Cancer
:
: FILE REFERENCE: 3380/11127-US4
:
: CURRENT APPLICATION NUMBER: US/09/R34,794A
:

```

;; PRIOR APPLICATION NUMBER: 09/146,580
;; PRIOR FILING DATE: 1998-09-03
;; PRIOR APPLICATION NUMBER: 60/071,899

;; PRIOR APPLICATION NUMBER: 60/092,155
;; PRIOR FILING DATE: 1998-07-09
;; NUMBER OF SEQ ID NOS: 35

```

;      SEQ ID NO 28
;      LENGTH: 99
;      TYPE: PRT

```

03-03-034-154A-20

Query Match	Score
-------------	-------

Qy 11 MKVSALLCLLMAATFSPQGLA

71 KEAVIFKTRGKEVCADPKERWV

SEARCH COMPLETED February 10 20

•

•

•

•

•

•

•

•

•

•

•

•

•

Query Match	62.48;	Score 354;	DB 9;	Length 99;
-------------	--------	------------	-------	------------

11 MKVSALLCLLMAATFSPQGLAPDSVIPITCCFNVINRKIPIORLESTRINIQCP 70

71 KEAVIEKTRGKEVCADPKERWVRDSMKHLDQIFONLK 108

Search completed: February 18, 2003 03:07:08

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2003, 03:00:21 ; Search time 40 Seconds

(without alignments)
261.966 Million cell updates/sec

Title: US-10-033-067-1

Perfect score: 567
Sequence: 1 MLKLTPLPSKMKVSNALLCL.....ERWVDSMKHLDIQRNLKP 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	513	90.5	99	2 JC5295	monocyte chemotact
2	372	65.6	99	2 JC2417	monocyte chemotact
3	367	64.7	99	2 A60299	monocyte chemotact
4	357	63.0	109	2 A54678	monocyte chemotact
5	349	61.6	97	2 JC4912	eotaxin precursor
6	339	59.8	99	2 JC2136	monocyte chemotact
7	302	53.3	99	1 A39296	monocyte chemotact
8	302	53.3	99	2 JC2336	monocyte chemotact
9	298	52.6	125	2 I46857	monocyte chemotact
10	280.5	45.5	96	2 I46099	eotaxin precursor
11	273.5	45.2	96	2 JC2478	eotaxin precursor
12	259	45.7	148	1 A30209	PDGF-inducible JE
13	255	45.0	120	2 I48147	monocyte chemotact
14	250	44.1	148	1 S07723	immediate-early se
15	244	43.0	97	2 A48093	monocyte cytokine
16	219	38.6	72	2 A55984	monocyte chemotact
17	183.5	33.4	93	2 B35673	LD78-beta protein
18	174.5	30.8	92	1 A31767	macrophage inflamm
19	169.5	29.9	92	2 C30552	macrophage inflamm
20	169.5	29.9	92	2 I46730	immune activation
21	163	28.7	92	2 A33933	macrophage inflamm
22	159	28.0	92	2 A30574	macrophage inflamm
23	158	27.9	92	2 I53322	macrophage inflamm
24	157	27.7	91	1 A28815	monocyte chemotact
25	149	26.3	91	1 A46539	monocyte chemotact
26	148.5	26.2	120	2 JE0177	lymphocyte and mon
27	136.5	24.1	96	2 A37236	I-309 protein prec
28	135.5	23.9	92	2 S24236	TCF3 protein - mon
29	127.5	22.5	114	1 ETRHUL	lymphotactin precu

30	118.5	20.9	114	1 ETRHUL	lymphotactin precu
31	104	18.3	50	2 C60407	monocyte adherence
32	97.5	17.2	116	2 I49555	gene C10 protein -
33	97	17.1	103	2 A53096	interleukin-8 prec
34	93	16.4	101	2 S42496	interleukin-8 prec
35	92	16.2	100	2 S46198	cytokine-induced n
36	90	15.9	117	2 B44253	alveolar macrophag
37	87	15.3	99	2 A37034	interleukin-8 prec
38	83.5	14.7	85	1 B30552	T-cell activation
39	83.5	14.7	98	1 TGHUGI	interferon gamma-i
40	83	14.6	95	2 JN0841	interleukin-8 - do
41	82	14.5	101	2 I48148	Neutrophil attract
42	81	14.3	132	2 A57325	C-X-C chemokine LI
43	80	14.1	101	2 I46871	interleukin-8 - ra
44	78	13.8	114	2 A55010	neutrophil-activat
45	75.5	13.3	100	2 JH0200	macrophage inflamm

ALIGNMENTS

RESULT 1
JC5295
monocyte chemotactic protein-2 precursor - human
C:Species: Homo sapiens (man)
C:Date: 02-May-1997 #sequence_revision 18-Jul-1997 #text_change 20-Jun-2000
C:Accession: JC5295
R:Van Coillie, E.; Froyen, G.; Nomiyama, H.; Miura, R.; Fitem, P.; Van Aelst, I.; Ve
Biochem. Biophys. Res. Commun. 231, 726-730, 1997
A:Title: Human monocyte chemotactic protein-2: cDNA cloning and regulated expression
A:Reference number: JC5295; MUID:9724420; PMID:9070881
A:Accession: JC5295
A:Molecule type: mRNA
A:Residues: 1-99 <VAN>
A:Cross-references: GB:Y10802; NID:q1924937; PIDN:CA71760.1; PID:q1924938
A:Experimental source: bone marrow
C:Comment: This protein belongs to the beta-chemokine family which is one of the major
ligands in tumor biology, and contribute to the trafficking and recruitment of the re
C:Genetics:
A:Gene: mcp-2
C:Superfamily: macrophage inflammatory protein
F:123/Domain: signal sequence #status predicted <SIG>
F:24-99/Product: monocyte chemotactic protein-2 #status predicted <MAT>

Query Match 90.5%; Score 513; DB 2; Length 99;
Best Local Similarity 99.0%; Pred. No. 4.4e-49;
Matches 98; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 11 MKVSALLCLLLMAFPSPGSLAPDSVSIPTCCFVNIKRIPIDRLESYTRITNIQCP 70
|||||
Db 1 MKVSALLCLLLMAFPSPGSLAPDSVSIPTCCFVNIKRIPIDRLESYTRITNIQCP 60
|||||

OY 71 KEAVIFKTRGKEVCADPKERWVDSMKHLDIQRNLKP 109
|||||
Db 61 KEAVIFKTRGKEVCADPKERWVDSMKHLDIQRNLKP 99
|||||

RESULT 2
JC2417
monocyte chemoattractant protein-2 precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 16-Jul-1999
C:Accession: JC2417
R:Hosang, K.; Knoke, I.; Kraudt, J.; Wempe, F.; Wutke, W.; Schelt, K.H.
Biochem. Biophys. Res. Commun. 205, 148-153, 1994
A:Title: Porcine luteal cells express monocyte chemoattractant protein-2 (MCP-2): Ar
A:Reference number: JC2417; MUID:95091716; PMID:7999015
A:Accession: JC2417
A:Molecule type: mRNA
A:Residues: 1-99 <HOS>
A:Cross-references: GB:248480; NID:q683718; PIDN:CA488371.1; PID:q683719
A:Experimental source: corpus luteum
C:Superfamily: macrophage inflammatory protein

	A:Residues:	1-109	<OPD>	
	A:Cross-references:	GB:X72308		
	B:Opdenaker,	G.; Froyen, G., Flten, P., Proost, P., Van Damme, J.		
	Biochim. Biophys. Res. Commun.	191, 535-542, 1993		
	A:Title:	Human monocyte chemotactic protein-3 (MCP-3): Molecular cloning of the cDNA and		
	A:Reference number:	JC1478; MUID:93213290; PMID:8461011		
	A:Accession:	JC1478		
	A:Molecule type:	mRNA		
	A:Residues:	1-109 <OPD>		
	A:Cross-references:	GB:X72308; GB:S57464; NID:g3328270; PIDN:CAA51055.1; PID:g313708		
	R:Minly, A.; Chalon, P.; Guillemot, J.C.; Kadhaf, M.; Liauzun, P.; Magazini, M.; Miloux,			
	submitted to the EMBL Data Library, March 1993			
	A:Description:	Molecular cloning of MCP-3: a human monocyte-derived monocyte chemoatrac		
	A:Reference number:	SJ32222		
	A:Accession:	SJ32222		
	A:Molecule type:	mRNA		
	A:Residues:	1-109 <MIN>		
	A:Cross-references:	EMBL:X71087; NID:g288396; PIDN:CAA50405.1; PID:g288397		
	C:Comment:	This protein induces proteinase secretion and chemotaxis by macrophages and n		
	C:Genetics:			
	A:Gene:	GDB:SCYA7; SCYA6; MCP-3		
	A:Map position:	17q11-17q12		
	A:Introns:	36/1; 75/2		
	C:Superfamily:	macrophage inflammatory protein		
	C:Keywords:	cytokine; glycoprotein; inflammation		
	F:1-33/Domains:	signal sequence #status predicted <SIG>		
	F:34-109/Product:	monocyte chemotactic protein 3 #status predicted <MAT>		
	F:39/Binding site:	carbohydrate (asn) (covalent) #status predicted		
Oy	Query Match	63.0%; Score 357; DB 2; Length 109;		
	Best Local Similarity	63.9%; Pred. No. 6.5e-32;		
Dd	Matches	69; Conservative 11; Mismatches 28; Indels 0; Gaps 0;		
Oy	1 MLKLPPLPSMKYSAALCLLLMAATFSPQGLAOPDSVIPITCCFNVNRKIPIORLES 60			
Dd	1 MMKPMPSPSMKKASALLCLLTAAAFSPQGLAPGVGINTSTGCCRYFKIRNKIPORLES 60			
Oy	61 YRRTINOCPEKAIVIFPKTRKGECADPKEERVRWRSDMKHLDFOIMLK 108			
Dd	61 YRRTSSHCRNAVIFRKTKDKELCADPTQKWVDPMRLHLDKKTQIPIK 108			
RESULT 5	JC4912			
	eotaxin precursor - human			
	C:Species:	Homo sapiens (man)		
	C>Date:	01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 20-Jun-2000		
	C:Accession:	JC4912		
	R:Bartheleis, J.; Schleuter, C.; Richter, E.; Noso, N.; Kulke, R.; Christophers, E.; Schroe			
	Biochim. Biophys. Res. Commun.	225, 1045-1051, 1996		
	A:Title:	Human dermal fibroblasts express eotaxin: Molecular cloning, mRNA expression, e		
	A:Reference number:	JC4912; MUID:96374440; PMID:8780731		
	A:Accession:	JC4912		
	A>Status:	preliminary		
	A:Molecule type:	mRNA		
	A:Residues:	1-97 <BAR>		
	A:Cross-references:	EMBL:Z75668; NID:g1531982; PIDN:CAA99997.1; PID:g1531983		
	A:Experimental source:	dermal fibroblast		
	C:Comment:	This protein has eosinophil specific chemotactic activity.		
	C:Superfamily:	macrophage inflammatory protein		
	C:Keywords:	fibroblast		
	F:1-18/Domains:	signal sequence #status predicted <SIG>		
	F:19-97/Product:	eotaxin #status predicted <MAT>		
Oy	Query Match	61.6%; Score 349; DB 2; Length 97;		
	Best Local Similarity	68.7%; Pred. No. 4.4e-31;		
Dd	Matches	68; Conservative 13; Mismatches 16; Indels 2; Gaps 1;		
Oy	11 MKYSAILLCILLMAATFSPQGLAOPDSVIPITCCFNVINRRIPIORLESYRITNTICP 70			
Dd	1 MKYSAILCWILLLIAATSPOGLTCP--ASVPITCGENLANRKIIPILORLFESYRITSCKP 58			

```

QY      71 KEAVIFKTRKGECVADPKERWVRDSMKHLDDQFONLKP 109
       1:::||||| 1:::|||||:|||||:|||||:||||| 11
Db      59 QKAVIFKTKLKARDICADPKRRKWVDMSKTYLDQKSPTPKP 97

RESULT 6
JC2136
monocyte chemoattractant protein-1 precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 16-Jul-1999
A:Accession: Jc2136; S57498
R:Hosang, K.; Knokke, I.; Klaidiny, J.; Wempe, F.; Mutlke, W.; Scheit, K.H.
Biochem. Biophys. Res. Commun. 199, 962-968, 1994
A>Title: Porcine luteal cells express monocyte chemoattractant protein-1 (MCP-1): An
A:Reference number: JC2136; MUID:94I83284; PMID:7510962
A:Accession: Jc2136
A:Molecule type: mRNA
A:Residues: 1-99 <HOS>
A:Cross-references: GB:I248479; NID:9683716; PIDN:CAA88370.1; PID:9683717
R:Zach, O.
submitted to the EMBL Data Library, July 1994
A:Reference number: S57497
A:Accession: S57498
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-99 <ZAC>
A:Cross-references: EMBL:X79416; NID:9872312; PIDN:CAAS54545.1; PID:9872313
C:Superfamily: macrophage inflammatory protein
C:Keywords: glycoprotein
F:1-73/Domain: signal sequence #status predicted <SIG>
F:74-99/Product: monocyte chemoattractant protein-1 #status predicted <MAT>
F:94/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          59.8%; Score 339; DB 2; Length 99;
Best Local Similarity 62.6%; Pred. No. 5,6e-30;
Matches    62; Conservative   19; Mismatches   18; Indels     0; Gaps     0;

QY      11 MKVSALLCLLLMAAFSPDGLAQDPDSVSPITPCGEENVIRKRPIQLLESTRTINTOCP 70
       |||||  |||||  |||||  |||||  ::|||:  :|||:  :|||  |||  |  |  |  |
Db      1  MKVSALLCLLLTAAFFCQVLAQPDAINSPVCCTYLTPSKISMORLSRYRVTSKCP 60

QY      71 KEAVIFKTRKGECVADPKERWVRDSMKHLDDQFONLKP 109
       |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      61 KEAVIFKTIAGKEICAPKKOKWQDSISHLDKKNQTFRP 99

RESULT 7
A39296
monocyte chemoattractant protein 1 precursor - bovine
N:Alternate names: monocyte chemotactic factor 1; seminal plasma protein P6
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
A:Accession: A39296; B39296
R:Wempe, F.; Henschen, A.; Scheit, K.H.
DNA Cell Biol. 10, 671-679, 1991
A>Title: Gene expression and cDNA cloning identified a major basic protein constitutively expressed in bovine neutrophils
A:Reference number: A39296; MUID:92096117; PMID:1721821
A:Accession: A39296
A:Molecule type: mRNA
A:Residues: 1-99 <WEM>
A:Cross-references: GB:M84602; GB:M85264; NID:9163394; PIDN:AAA30651.1; PID:9163395
A:Accession: B39296
A:Molecule type: protein
A:Residues: 50-68,'X','70-74','X','76 <WE2>
A:Experimental source: seminal vesicle
C:Superfamily: macrophage inflammatory protein
C:Keywords: glycoprotein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-99/Product: monocyte chemoattractant protein 1 #status predicted <MAT>
F:94/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          53.3%; Score 302; DB 1; Length 99;
Best Local Similarity 56.6%; Pred. No. 6,5e-26;

```


F:29/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 43.0%; Score 244; DB 2; Length 97;

Best Local Similarity 51.5%; Pred. No. 1.5e-19;

Matches 51; Conservative 18; Mismatches 28; Indels 2; Gaps 2;

```
QY 11 MKVSALLCLLMATFSPQGLAOPDSYSIPITCCFNVINRKIPIQRLSEYTRITNIQCP 70
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MRISATLLCLLLIAAFSIQYWAQPDGPNAS-TCCY-VKKQKIPKRNLSYRRTISSRCP 58
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 71 KEAVIFKTKRGEVCADPKERWVRDSDKHLDQIFONLKP 109
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 59 WEAVIFKTKRGEVCRAHQKWEAEALAYLDMKTPPTPKP 97
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Search completed: February 18, 2003, 03:05:57

Job time : 41 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2003, 01:57:56 ; Search time 22 Seconds

(without alignments)
205.496 Million cell updates/sec

Title: US-10-033-067-1

Perfect score: 567
Sequence: 1 MKKLPLPSKMKYSALLCL.....ERWVDSMKHLIDIFONLKP 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	517	91.2	99	1 SY08_HUMAN	P80075 homo sapien
2	382	67.4	99	1 SY02_MACFA	O9494 macaca fasc
3	372	65.6	99	1 SY08_PIG	P49873 sus scrofa
4	367	64.7	99	1 SY02_HUMAN	P13500 homo sapien
5	359	63.3	99	1 SY08_BOVIN	O09141 bos taurus
6	350	61.7	97	1 E07A_HUMAN	P51671 homo sapien
7	339	59.8	99	1 SY02_PIG	P42831 sus scrofa
8	337	59.4	99	1 SY07_HUMAN	P80098 homo sapien
9	328.5	57.9	98	1 SY13_HUMAN	O90616 homo sapien
10	327	57.7	101	1 SY12_CANFA	O62401 mus musculu
11	319.5	56.3	104	1 SY02_MOUSE	P52203 canis famli
12	302	53.3	99	1 MCPB_BOVIN	P28292 oryctolagus
13	298	52.6	125	1 SY02_RABIT	P28292 oryctolagus
14	283	49.9	97	1 E07A_RAT	P97545 rattus norv
15	282	49.7	97	1 SY08_MOUSE	O94121 mus musculu
16	280.5	49.5	96	1 E07A_CAVPO	P48298 mus musculu
17	270	47.6	97	1 E07A_MOUSE	P10148 mus musculu
18	259	45.7	148	1 SY02_MOUSE	O08782 cavia porce
19	255	45.0	120	1 SY02_CAVPO	P18444 rattus norv
20	250	44.1	148	1 SY02_RAT	O03366 mus musculu
21	249	43.9	97	1 SY07_MOUSE	P80325 bos taurus
22	239	42.2	74	1 MCPB_BOVIN	O9494 macaca fasc
23	239	42.2	97	1 SY07_RAT	O9494 macaca fasc
24	185.5	32.7	90	1 SY04_CHICK	P16619 homo sapien
25	183.5	32.4	93	1 SY04_HUMAN	P13236 h small ind
26	174.5	30.8	92	1 SY04_HUMAN	O9494 macaca fasc
27	172.5	30.4	119	1 SY04_MOUSE	P14097 mus musculu
28	169.5	29.9	92	1 SY04_MOUSE	P46632 oryctolagus
29	169.5	29.9	119	1 SY04_RABIT	O00175 homo sapien
30	166.5	29.0	119	1 SY04_HUMAN	P82943 bos taurus
31	164.5	29.0	70	1 REG1_BOVIN	P97272 cavia porce
32	163	28.7	91	1 SY05_CAVPO	P10855 mus musculu
33	163	28.7	92	1 SY03_MOUSE	

34	162.5	28.7	92	1 SY04_RAT	P50230 rattus norv
35	159	28.0	92	1 SY03_HUMAN	P10147 homo sapien
36	158	27.9	92	1 SY03_RAT	P50229 rattus norv
37	157	27.7	91	1 SY05_HUMAN	P13501 homo sapien
38	156	27.5	91	1 SY05_BOVIN	O97919 bos taurus
39	155	27.3	93	1 SY14_HUMAN	O16627 mus musculu
40	149	26.3	91	1 SY05_MOUSE	P30882 mus musculu
41	148.5	26.2	120	1 SY16_HUMAN	O15467 h small ind
42	144	25.4	113	1 SY15_HUMAN	O16663 homo sapien
43	140.5	24.8	120	1 SY23_HUMAN	P55773 homo sapien
44	139.5	24.6	92	1 SY05_RAT	P50231 rattus norv
45	136.5	24.1	96	1 SY01_HUMAN	P22362 homo sapien

ALIGNMENTS

RESULT 1
ID SY08_HUMAN STANDARD: PRT: 99 AA.
AC P80075; P78388;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Small inducible cytokine A8 precursor (CCL8) (Monocyte chemotactic protein 2) (MCP-2) (Monocyte chemoattractant protein 2) (HCL4).
DE SCYA8 OR SCYA10 OR MCP2.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=97237052; PubMed=9119400;
RA van Coillie E., Fiten P., Nomiyama H., Sakaki Y., Miura R., Yoshie O., van Damme J., Opdenakker G.;
RT "The human MCP-2 gene (SCYA8): cloning, sequence analysis, tissue expression, and assignment to the CC chemokine gene contig on chromosome 17q11.2.";
RT Genomics 40:323-331(1997).
RN [2]
RP MEDLINE=97224420; PubMed=9070881;
RA van Coillie E., Froyen F., Nomiyama H., Miura R., Fiten P., van Aelst I., van Damme J., Opdenakker G.;
RT "Human monocyte chemotactic protein-2: cDNA cloning and regulated expression of mRNA in mesenchymal cells.";
RT Biochem. Biophys. Res. Commun. 231:726-730(1997).
RN [3]
RP MEDLINE=91207938; PubMed=2518726;
RA Chang H.C., Hsu F., Freeman G.J., Griffin J.D., Reinherz E.L.;
RT "Cloning and expression of a gamma-interferon-inducible gene in monocytes: a new member of a cytokine gene family.";
RT Int. Immunol. 1:388-399(1989).
RN [4]
RP MEDLINE=97053697; PubMed=8898111;
RA Kim K.-S., Rajaratnam K., Clark-Lewis I., Sykes B.D.;
RT "Structural characterization of a monomeric chemokine: monocyte chemoattractant protein-3.";
RT FEBS Lett. 359:277-282(1996).
CC -!- FUNCTION: CHEMOTACTIC FACTOR THAT ATTRACTS MONOCYTES, LYMPHOCYTES,


```

CC BASOPHILS AND EOSINOPHILS. MAY PLAY A ROLE IN NEOPLASIA AND
CC INFAMMATORY HOST RESPONSES. THIS PROTEIN CAN BIND HEPARIN.
CC -1- SUBUNIT: MONOMER OR HOMODIMER; IN EQUILIBRIUM.
CC -1- TISSUE SPECIFICITY: HIGHEST EXPRESSION FOUND IN THE SMALL
CC INTESTINE AND PERIPHERAL BLOOD CELLS. INTERMEDIATE LEVELS SEEN IN
CC THE HEART, PLACENTA, LUNG, SKELETAL MUSCLE, THYMUS, COLON, OVARY,
CC SPINAL CORD AND PANCREAS. LOW LEVELS SEEN IN THE BRAIN, LIVER,
CC SPLEEN AND PROSTATE.
CC -1- INDUCTION: BY INTERFERON GAMMA, MITOGENS AND INTERLEUKIN-1.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X99886; CAA68168.1; ALT_INIT.
CC DR EMBL: Y10802; CAA71760.1; -.
CC DR EMBL: Y16645; CAA76341.1; -.
CC DR HSSP: P51671; IEOT.
CC DR Genew: HGNC:10635; SCYA8.
CC DR MIM: 602283; -.
CC DR InterPro: IPR000827; CC_chemkine_sml.
CC DR InterPro: IPR001811; Chemokine_IL8.
CC DR Pfam: PF00048; IL8; 1.
CC DR SMART: SM00199; SCY; 1.
CC DR PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
CC KW Cytokine; Chemotaxis; Signal; Heparin-binding; Inflammatory response;
CC Polymorphism.
CC FT SIGNAL 1 23 PROBABLE.
CC FT CHAIN 24 99 SMALL INDUCIBLE CYTOKINE A8.
CC FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID.
CC FT DISULFID 34 59 BY SIMILARITY.
CC FT DISULFID 35 75 BY SIMILARITY.
CC FT VARIANT 69 69 K->O.
CC FT /FTID-VAR-001633.
CC SQ SEQUENCE 99 AA; 11246 MW; 9D67976BB9422F2A CRC64;
CC -----
Query Match 91.2%; Score 517; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.6e-50;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 MKVSAALLCLLLMAATFSPGGLAOPDSVSIPTCCFNVINRKIPQRLSEYTRITNIQCP 70
DB 1 MKVSAALLCLLLMAATFSPGGLAOPDSVSIPTCCFNVINRKIPQRLSEYTRITNIQCP 60
QY 71 KEAVIFKTRKRGKVCADPKERWVDSKHLDOIIFONLKP 109
DB 61 KEAVIFKTRKRGKVCADPKERWVDSKHLDOIIFONLKP 99

```

```

RESULT 2
SY02_MACFA STANDARD; PRT; 99 AA.
ID SY02_MACFA
AC 09MYN4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Small inducible cytokine A2 precursor (CC12) (Monocyte chemotactic
DE protein 1) (MCP-1) (Monocyte chemoattractant protein-1).
GN SCYA2 OR MCP1.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cetartiodactyla; Macaca.
OC NCBL_TaxID=9541, 9544;
[1]
RP SEQUENCE FROM N.A.

```

```

RC SPECIES=M.fascicularis;
RA Studer C., Ufer R.;
RT "Cloning and expression of cynomolgus monkey chemoattractant
RT protein-1."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN 121
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta;
RA Studer C., Ufer R.;
RT "Cloning and expression of rhesus monkey monocyte chemoattractant
RT protein-1."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CHEMOTACTIC FACTOR THAT ATTRACTS MONOCYTES AND BASOPHILS
CC BUT NOT NEUTROPHILS OR EOSINOPHILS. BINDS TO CCR2 AND CCR4 (BY
CC SIMILARITY).
CC -1- SUBUNIT: MONOMER OR HOMODIMER; IN EQUILIBRIUM (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF276081; AAF81899.1; -.
CC DR EMBL: AF255343; AAF67756.1; -.
CC DR HSSP: P13500; IDOK.
CC DR InterPro: IPR000827; CC_chemkine_sml.
CC DR InterPro: IPR001811; Chemokine_IL8.
CC DR Pfam: PF00048; IL8; 1.
CC DR SMART: SM00199; SCY; 1.
CC DR PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
CC KW Cytokine; Chemotaxis; Signal; Inflammatory response.
CC FT SIGNAL 1 23 BY SIMILARITY.
CC FT CHAIN 24 99 SMALL INDUCIBLE CYTOKINE A2.
CC FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID (BY
CC SIMILARITY).
CC FT DISULFID 34 59 BY SIMILARITY.
CC FT DISULFID 35 75 BY SIMILARITY.
CC FT CARBOHYD 37 37 N-LINKED (GLCNAC. ...) (POTENTIAL).
CC SQ SEQUENCE 99 AA; 11007 MW; 433CB88C4EE7A4F CRC64;
CC -----
Query Match 67.4%; Score 382; DB 1; Length 99;
Best Local Similarity 70.7%; Pred. No. 1.5e-35;
Matches 70; Conservative 14; Mismatches 15; Indels 0; Gaps 0;
QY 11 MKVSAALLCLLLMAATFSPGGLAOPDSVSIPTCCFNVINRKIPQRLSEYTRITNIQCP 70
DB 1 MKVSAALLCLLLMAATFSPGGLAOPDAINAPVTCYNTNRKISVQRLASRRITSSKCP 60
QY 71 KEAVIFKTRKRGKVCADPKERWVDSKHLDOIIFONLKP 109
DB 61 KEAVIFKTRKRGKVCADPKERWVDSKHLDOIIFONLKP 99

```

```

RESULT 3
SY08_PIG STANDARD; PRT; 99 AA.
ID SY08_PIG
AC P49873;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Small inducible cytokine A8 precursor (CC18) (Monocyte chemotactic
DE protein 2) (MCP-2) (Monocyte chemoattractant protein 2).
GN SCYA8 OR MCP2.
OS Sus scrofa (Pig).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC NCBL_TaxID=9823;

```


RP SEQUENCE OF 29-53 AND 82-92.
 RA MEDLINE-90211336; PubMed-2322286;
 RT Decock B., Conings R., Lenaerts J.-P., Billiau A., Van Damme J.;
 RT "Identification of the monocyte chemotactic protein from human
 RT osteosarcoma cells and monocytes: detection of a novel N-terminally
 RT processed form.";
 RL Biochem. Biophys. Res. Commun. 167:904-909(1990).
 RN [12]
 RP 3D-STRUCTURE MODELING.
 RA MEDLINE-91312872; PubMed-1857712;
 RT Gronenborn A.M., Clore G.M.;
 RT "Modeling the three-dimensional structure of the monocyte chemo-
 RT attractant and activating protein MCP-1 on the basis of the
 RT solution structure of interleukin-8.";
 RL Protein Eng. 4:263-269(1991).
 RN [13]
 RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).
 RA MEDLINE-97143315; PubMed-8989326;
 RT Lubkowski J., Bujacz G., Domaille P.J., Handel T.M., Wlodawer A.;
 RT "The structure of MCP-1 in two crystal forms provides a rare example
 RT of variable quaternary interactions.";
 RL Nat. Struct. Biol. 4:64-69(1997).
 RN [14]
 RP STRUCTURE BY NMR.
 RA MEDLINE-96234959; PubMed-8639605;
 RT Handel T.M., Domaille P.J.;
 RT "Heteronuclear (1H, 13C, 15N) NMR assignments and solution structure
 RT of the monocyte chemotactic protein-1 (MCP-1) dimer.";
 RL Biochemistry 35:6569-6584(1996).
 RN [15]
 RP EFFECT OF DELETION OF N-TERMINAL RESIDUES.
 RA MEDLINE-96195223; PubMed-8627182;
 RT Weber M., Unguccio M., Baggiolini M., Clark-Lewis I., Dahinden C.A.;
 RT "Deletion of the NH2-terminal residue converts monocyte chemotactic
 RT protein 1 from an activator of basophil mediator release to an
 RT eosinophil chemottractant.";
 RL J. Exp. Med. 183:681-685(1996).
 RN [16]
 RP MUTAGENESIS.
 RA MEDLINE-94253189; PubMed-8195247;
 RT Zhang Y.J., Rutledge B.J., Rollins B.J.;
 RT "Structure/activity analysis of human monocyte chemoattractant
 RT protein-1 (MCP-1) by mutagenesis. Identification of a mutated protein
 RT that inhibits MCP-1-mediated monocyte chemotaxis.";
 RL J. Biol. Chem. 269:15918-15924(1994).
 RN [17]
 RP SUBUNIT.
 RA MEDLINE-97053697; PubMed-8898111;
 RA Kim K.-S., Rajaratnam K., Clark-Lewis I., Sykes B.D.;
 RT "Structural characterization of a monomeric chemokine: monocyte
 RT chemoattractant protein-3.";
 RL FEBS Lett. 395:277-282(1996).
 CC -1- FUNCTION: CHEMOTACTIC FACTOR THAT ATTRACTS MONOCYTES AND BASOPHILS
 CC BUT NOT NEUTROPHILS OR EOSINOPHILS. AUGMENTS MONOCYTE ANTI-TUMOR
 CC ACTIVITY. HAS BEEN IMPLICATED IN THE PATHOGENESIS OF DISEASES
 CC CHARACTERIZED BY MONOCYTIC INFILTRATES, LIKE PSORIASIS, RHEUMATOID
 CC ARTHRITIS OR ATHEROSCLEROSIS. MAY BE INVOLVED IN THE RECRUITMENT
 CC OF MONOCYTES INTO THE ARTERIAL WALL DURING THE DISEASE PROCESS OF
 CC ATHEROSCLEROSIS. BINDS TO CCR2 AND CCR4.
 CC -1- SUBUNIT: MONOMER OR HOMODIMER. IN EQUILIBRIUM.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: PROCESSING AT THE N-TERMINUS CAN REGULATE RECEPTOR AND TARGET
 CC CELL SELECTIVITY. DELETION OF THE N-TERMINAL RESIDUE CONVERTS
 CC IT FROM AN ACTIVATOR OF BASOPHIL TO AN EOSINOPHIL CHEMOTTRACTANT.
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
 CC C-C) (CHEMOKINE CC).
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)

CC or send an email to license@isb.ch.
 CC -----
 DR EMBL: M31626; AAA36330.1; -
 DR EMBL: M30816; AAA36330.1; JOINED.
 DR EMBL: M31625; AAA36330.1; JOINED.
 DR EMBL: M24545; AAA18164.1; -
 DR EMBL: M28226; AAA60309.1; -
 DR EMBL: X14768; AAA32876.1; -
 DR EMBL: M37719; AAA18102.1; -
 DR EMBL: M28225; AAA60308.1; -
 DR EMBL: M28223; AAA60308.1; JOINED.
 DR EMBL: M28224; AAA60308.1; JOINED.
 DR EMBL: S69738; AAB29226.1; -
 DR EMBL: S71513; AAB20651.1; -
 DR EMBL: Y18933; CAC10409.1; -
 DR EMBL: A17786; CAA01352.1; -
 DR PIR: A35474; A35474.
 DR PIR: S03339; S03339.
 DR PDB: IDOK; 12-MAR-97.
 DR PDB: IDOL; 12-MAR-97.
 DR PDB: IDOM; 14-OCT-96.
 DR PDB: IDON; 14-OCT-96.
 DR PDB: IMCA; 15-OCT-94.
 DR GeneW; HGNC:10618; SCY1A2.
 DR MIM: 158105; -
 DR InterPro: IPR000827; CC_Chemkine.sml.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR Pfam: PF00048; IL8; 1.
 DR SMART; SM00199; SCY; 1.
 DR PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
 DR KEGG; Cytokine; Chemotaxis; Signal; Inflammatory response; 3D-structure.
 FT SIGNAL 1 23
 FT CHAIN 24 99 SMALL INDUCIBLE CYTOKINE A2.
 FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID.
 Query Match 64.7%; Score 367; DB 1; Length 99;
 Best Local Similarity 69.4%; Pred. No. 6,9e-34;
 Matches 68; Conservative 14; Mismatches 16; Indels 0; Gaps 0;
 Oy 11 MKVSALLCLLLMATAFSPQGLAOPDSVSIPTCCNVINRKIPIDLESTRTITNOCP 70
 Db 1 MKVSALLCLLLMATAFSPQGLAOPDAIPVCCVFNTRKISVORLSTRITSSKCP 60
 Oy 71 KEAVIFKTKRKEVCADPKERNWRDMSKRIIDQIFQMLK 108
 Db 61 KEAVIFKTIKAEICADPKRQKNVQDSMDHLDKOTQTPK 98
 RESULT 5
 SY08_BOVIN STANDARD; PRT; 99 AA.
 AC 009141.
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Small inducible cytokine A8 precursor (CCL8) (Monocyte chemotactic
 DE protein 2) (MCP-2) (Monocyte chemoattractant protein 2).
 GN SCY1A8 OR MCP2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [11]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-94114084; PubMed-8286035;
 RA Wempe F., Hanes J., Scheit K.H.;
 RT "Cloning of the gene for bovine monocyte chemoattractant protein-2.";
 RL DNA Cell Biol. 13:1-8(1994).
 CC -1- FUNCTION: CHEMOTACTIC FACTOR THAT ATTRACTS MONOCYTES. THIS PROTEIN
 CC CAN BIND HEPARIN.
 CC -1- SUBUNIT: MONOMER OR HOMODIMER. IN EQUILIBRIUM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE

CC C-C) (CHEMOKINE CC).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: S67954; AAD14005.1; -
CC EMBL: S67956; AAB29750.1; -
CC HSSP: P51671; 1EOP.
CC InterPro: IPR000827; CC_chemokine_sml.
CC InterPro: IPR001811; Chemokine_IL8.
CC Pfam: PF00048; IL8; 1.
CC SMART: SM00199; SCY; 1.
CC PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
CC Cytokine; Chemotaxis; Signal; Heparin-binding; Inflammatory response.
CC SIGNAL.
CC FT CHAIN 1 23 BY SIMILARITY.
CC FT MOD_RES 24 24 PYROLIDONE CARBOXYLIC ACID (BY
CC FT SIMILARITY).
CC FT DISULFID 34 59 BY SIMILARITY.
CC FT DISULFID 35 75 BY SIMILARITY.
CC SQ SEQUENCE 99 AA; 10900 MW; 01974CDB3FF9119B CRC64;

Query Match 63.3%; Score 359; DB 1; Length 99;
Best local Similarity 68.7%; Pred. No. 5.3e-33;
Matches 68; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 11 MKVSALLCLLMATFSPQGLAOPDSVSIPTCCFNVINKRIPQIRLESYTRITNICP 70
DB 1 MKVSAGLCLLVATGTQVLAPDSVPTTCFVSINKRIPKIDSTRINSQCP 60
QY 71 KEAVIFKTKRKEVCADPKERWRDMSKHLDTQIFONLKP 109
DB 61 QEAVIFKTKADRVCAADPKRQKQVOTISRLDQKSRTPKP 99

RESULT 6
EOTL_HUMAN STANDARD; PRT; 97 AA.
AC P51671; P50877; Q92490; Q92491;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Eotaxin precursor (Small inducible cytokine A11) (CCIL1) (Eosinophil
DE chemotactic protein).
GN SCY11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC NCBI_TaxID=9606;
OX [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96181758; PubMed=8597956;
RA Garcia-Zepeda E.A., Rothenberg M.E., Ownbey T.R., Leder P.,
RA Luster A.D.;
RT "Human eotaxin is a specific chemoattractant for eosinophil cells and
RT provides a new mechanism to explain tissue eosinophilia.";
RL Nat. Med. 2:449-456(1996).
RN [12]
RP SEQUENCE FROM N.A.
RX MEDLINE=96189937; PubMed=8609214;
RA Ponath P.D., Qin S., Ringler D.J., Clark-Lewis I., Wang J., Kassam N.,
RA Smith H., Shi X., Gonzalo J.A., Newman W., Gutierrez-Ramos J.C.,
RA Mackay C.R.;
RT "Cloning of the human eosinophil chemoattractant, eotaxin. Expression,
RT receptor binding, and functional properties suggest a mechanism for
RT the selective recruitment of eosinophils.";
RL J. Clin. Invest. 97:604-612(1996).
RN [3]

RP SEQUENCE FROM N.A.
RC TISSUE=Small intestine;
RX MEDLINE=96205964; PubMed=8631813;
RA Kitaura M., Nakajima T., Imai T.,
RA Kitaura H., Murphy P.M., Yoshie O.;
RT "Molecular cloning of human eotaxin, an eosinophil-selective CC
RT chemokine, and identification of a specific eosinophil eotaxin
RT receptor, CC chemokine receptor 3.";
RL J. Biol. Chem. 271:7725-7730(1996).
RN [14]
RP SEQUENCE FROM N.A., SEQUENCE OF 60-65 AND 75-88, AND VARIANTS.
RC TISSUE=Fore skin;
RX MEDLINE=96374440; PubMed=8780731;
RA Bartels J., Schuster C., Richter E., Noso N., Kulke R.,
RA Christophers E., Schroeder J.M.;
RT "Human dermal fibroblasts express eotaxin: molecular cloning, mRNA
RT expression, and identification of eotaxin sequence variants.";
RL Biochem. Biophys. Res. Commun. 225:1045-1051(1996).
RN [15]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=97312708; PubMed=9169149;
RA Garcia-Zepeda E.A., Rothenberg M.E., Wermowicz S., Sarafi M.N.,
RA Morton C.C., Luster A.D.;
RT "Genomic organization, complete sequence, and chromosomal location of
RT the gene for human eotaxin (SCY11), an eosinophil-specific CC
RT chemokine.";
RL Genomics 41:471-476(1997).
RN [16]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=97445071; PubMed=9299399;
RA Hein H., Schuster C., Kulke R., Christophers E., Schroeder J.M.,
RA Bartels J.;
RT "Genomic organization, sequence, and transcriptional regulation of
RT the human eotaxin gene.";
RL Biochem. Biophys. Res. Commun. 237:537-542(1997).
RN [17]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX Strausberg R.;
RT Submitted (Dec-2001) to the EMBL/GenBank/DBJ databases.
RN [18]
RP CARBOHYDRATE-LINKAGE SITE.
RC TISSUE=Blood;
RX MEDLINE=98237580; PubMed=9578468;
RA Noso N., Bartels J., Mallet A.I., Mochizuki M., Christophers E.,
RA Schroeder J.M.;
RT "Delayed production of biologically active O-glycosylated forms of
RT human eotaxin by tumor-necrosis-factor-alpha-stimulated dermal
RT fibroblasts.";
RL Eur. J. Biochem. 253:114-122(1998).
RN [19]
RP STRUCTURE BY NMR.
RX MEDLINE=98380469; PubMed=9712872;
RA Crump M.P., Rajarathnam K., Kim K.S., Clark-Lewis I., Sykes B.D.;
RT "Solution structure of eotaxin, a chemokine that selectively recruits
RT eosinophils in allergic inflammation.";
RL J. Biol. Chem. 273:22471-22479(1998).
RN [20]
RP FUNCTION: IN RESPONSE TO THE PRESENCE OF ALLERGENS, THIS PROTEIN
RP DIRECTLY PROMOTES THE ACCUMULATION OF EOSINOPHILS, A PROMINENT
RP FEATURE OF ALLERGIC INFLAMMATORY REACTIONS. BINDS TO CCR3.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- INDUCTION: BY TNF-ALPHA, INTERLEUKIN-1 ALPHA AND INTERFERON GAMMA.
CC -1- PTM: O-LINKED GLYCAN CONSISTS OF A GAL-GALNAc DISACCHARIDE WHICH
CC IS MODIFIED WITH UP TO 2 SIALIC ACID RESIDUES.
CC -1- SIMILARITY: BELONGS TO THE INTERCERIN BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
CC -1- DATABASE: NAME=R&D Systems' cytokine source book: SCY11;
CC WWW="http://www.rndsystems.com/asp/g_slebuilder.asp?bodyId=196".
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; U46573; AAA98957.1; -
 DR EMBL; U34780; AAC50369.1; -
 DR EMBL; DA9372; BAA08370.1; -
 DR EMBL; Z69291; CAA93258.1; -
 DR EMBL; Z75668; CAA98997.1; -
 DR EMBL; Z75669; CAA99998.1; -
 DR EMBL; U46572; AAC51297.1; -
 DR EMBL; Z92709; CAB07027.1; -
 DR EMBL; BC017850; AAH17850.1; -
 DR PDB; 1EOT; 13-JUN-99.
 DR PDB; 2EOT; 11-NOV-98.
 DR Genew; HGNC:10610; SCYA11.
 DR MIM; 601156; -
 DR Interpro: IPR000827; CC_chemkine_sml.
 DR Interpro: IPR001811; Chemokine_IL8.
 DR Pfam; PF00048; IL8; 1.
 DR SMART; SM00199; SCY; 1.
 DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
 DR Eosinophil; Cytokine; Chemotaxis; Glycoprotein; Signal;
 KW Inflammatory response; Polymorphism; 3D-structure.
 KW SIGNAL 1 23
 FT CHAIN 24 97 EOTAXIN.
 FT DISULFID 32 57
 FT DISULFID 33 73
 FT CARBOHYD 94 94
 FT VARIANT 7 7
 FT VARIANT 23 23
 FT VARIANT 51 51
 FT VARIANT 79 79
 FT SEQUENCE 97 AA; 10732 MW; B43C30FDACT1A7 CRC64;
 SQ

Query Match 61.7%; Score 350; DB 1; Length 97;
 Best Local Similarity 68.7%; Pred. No. 5,2e-32;
 Matches 68; Conservative 14; Mismatches 15; Indels 2; Gaps 1;

QY 11 MKVSALLCLLMAATFSPQGLAOPDSVIPITCCFVNRKIPIDQLESYRITNIQCP 70
 DB 1 MKVSALLCLLMAATFSPQGLAOP--ASVPTCCFNLNRKIPIDQLESYRITGKCP 58
 QY 71 KEAVIFKTRKKEVCADPKERKVRDSMKHLDQIFONLKP 109
 DB 59 OKAVIFKTRKLANDICADPKRKWVODSMKYLDOKSPTPKP 97

RESULT 7
 ST02_PIG STANDARD; PRT; 99 AA.
 ID SY02_PIG
 AC P42831;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemotactic
 DE protein 1) (MCP-1) (Monocyte chemoattractant protein-1).
 GN SCYA2.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94183284; PubMed=7510962;
 RA Hosang K., Knöke I., Klaudiny J., Wempe F., Wuttke K.H.,
 RT "Porcine luteal cells express monocyte chemoattractant protein-1"

RT (MCP-1): analysis by polymerase chain reaction and cDNA cloning.";
 RL Biochem. Biophys. Res. Commun. 199:962-968(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Zach O.R.F.;
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CHEMOTACTIC FACTOR THAT ATTRACTS MONOCYTES, BUT NOT
 CC NEUTROPHILS.
 CC -1- SUBUNIT: MONOMER OR HOMODIMER. IN EQUILIBRIUM (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
 CC C-C) (CHEMOKINE CC).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; Z48479; CAA88370.1; -
 DR EMBL; X79416; CAA55945.1; -
 DR HSSP; P13500; IDOM.
 DR Interpro: IPR000827; CC_chemkine_sml.
 DR Interpro: IPR001811; Chemokine_IL8.
 DR Pfam; PF00048; IL8; 1.
 DR SMART; SM00199; SCY; 1.
 DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
 KW Cytokine; Chemotaxis; Signal; Inflammatory response.
 KW SIGNAL 1 23
 FT CHAIN 24 99
 FT MOD_RES 24 24
 FT DISULFID 34 59
 FT DISULFID 35 75
 FT SEQUENCE 99 AA; 10976 MW; 4C0AC6278DAF0A09 CRC64;
 SQ

Query Match 59.8%; Score 339; DB 1; Length 99;
 Best Local Similarity 62.6%; Pred. No. 8,7e-31;
 Matches 62; Conservative 19; Mismatches 18; Indels 0; Gaps 0;

QY 11 MKVSALLCLLMAATFSPQGLAOPDSVIPITCCFVNRKIPIDQLESYRITNIQCP 70
 DB 1 MKVSALLCLLMAATFSPQGLAOPDAINSPVCCYLTGKISMOTLSYRVTSSKCP 60
 QY 71 KEAVIFKTRKKEVCADPKERKVRDSMKHLDQIFONLKP 109
 DB 61 KEAVIFKTRKKEVCADPKERKVRDSMKHLDQIFONLKP 99

RESULT 8
 SY07_HUMAN STANDARD; PRT; 99 AA.
 ID SY07_HUMAN
 AC P80098;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Small inducible cytokine A7 precursor (CCL7) (Monocyte chemotactic
 DE protein 3) (MCP-3) (Monocyte chemoattractant protein 3) (NC28).
 GN SCYA7 OR MCP3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. AND SEQUENCE OF 31-67 AND 71-99.
 RX MEDLINE=93213290; PubMed=8461011;
 RA Opdenakker G., Froyen G., Fiten P., Proost P., van Damme J.;
 RT "Human monocyte chemotactic protein-3 (MCP-3): molecular cloning of
 RT the cDNA and comparison with other chemokines.";
 RL Biochem. Biophys. Res. Commun. 191:535-542(1993).

RN [2]
 RX SEQUENCE FROM N.A.
 RA MEDLINE-94375065; PubMed-7916328;
 RA Opdenakker G., Fiten P., Nys G., Froyen G., van Roy N., Speleman F.,
 RA Laureys G., van Damme J.;
 RT "The human MCP-3 gene (SCYA7): cloning, sequence analysis, and
 RT assignment to the C-C chemokine gene cluster on chromosome
 RT 17q11.2-q12.";
 RL Genomics 21:403-408(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-93305913; PubMed-8318676;
 RA Minty A., Chalon P., Guillemot J.C., Kaghed M., Liaunus P.,
 RA Magasin M., Miloux B., Minty C., Ramond P., Vile N., Lupker J.,
 RA Shire D., Ferrara P., Caput D.;
 RT "Molecular cloning of the MCP-3 chemokine gene and regulation of its
 RT expression.";
 RL Eur. Cytokine Netw. 4:99-110(1993).
 RN [4]
 RP SEQUENCE OF 24-99 FROM N.A.
 RA Jang J.S., Kim B.E.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 30-99.
 RC TISSUE-Osteosarcoma;
 RA MEDLINE-92308855; PubMed-1613466;
 RA van Damme J., Proost P., Lenaerts J.-P., Opdenakker G.;
 RT "Structural and functional identification of two human, tumor-derived
 RT monocyte chemotactic proteins (MCP-2 and MCP-3) belonging to the
 RT chemokine family.";
 RL J. Exp. Med. 176:59-65(1992).
 RN [6]
 RP STRUCTURE BY NMR, AND SUBUNIT.
 RX MEDLINE-97053697; PubMed-8898111;
 RA Kim K.-S., Rajarathnam K., Clark-Lewis I., Sykes B.D.;
 RT "Structural characterization of a monomeric chemokine: monocyte
 RT chemottractant protein-3.";
 RL FEBS Lett. 395:277-282(1996).
 RN [7]
 RP STRUCTURE BY NMR.
 RX MEDLINE-97263733; PubMed-9109648;
 RA Meunier S., Bernassau J.-M., Guillemot J.-C., Ferrara P., Darbon H.;
 RT "Determination of the three-dimensional structure of CC chemokine
 RT monocyte chemoattractant protein 3 by 1H-two-dimensional NMR
 RT spectroscopy.";
 RL Biochemistry 36:4412-4422(1997).
 RN [8]
 RP STRUCTURE BY NMR.
 RA Kwon D., Lee D., Sykes B.D., Kim K.-S.;
 RL Submitted (AUG-1998) to the PDB data bank.
 CC -1- FUNCTION: CHEMOTACTIC FACTOR THAT ATTRACTS MONOCYTES AND
 CC EOSINOPHILS, BUT NOT NEUTROPHILS. AUGMENTS MONOCYTE ANTI-TUMOR
 CC ACTIVITY. ALSO INDUCES THE RELEASE OF GELATINASE B. THIS PROTEIN
 CC CAN BIND HEPARIN. BINDS TO CCR1, CCR2 AND CCR3.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: O-GLYCOSYLATED.
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
 CC C-C) (CHEMOKINE CC).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X72308; CAA51055.1; ALT_INT.
 DR EMBL: X72309; NOT_ANNOTATED_CDS.
 DR EMBL: X71087; CAA50407.1;
 DR EMBL: X71087; CAA50406.1; ALT_INT.
 DR EMBL: X71087; CAA50405.1; ALT_INT.

DR EMBL: AF043338; AAC03538.1;
 DR PIR: JC1478; JC1478.
 DR PIR: S32222; S32222.
 DR PIR: A54678; A54678.
 DR PIR: INCV; 15-OCT-97.
 DR PDB: 1BOC; 10-OCT-99.
 DR PDB: 1BOC; 10-OCT-99.
 DR GeneW: HGNC:10634; SCYA7.
 DR MIM: 158106;
 DR InterPro: IPR000827; CC_chemokine_sml.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR Pfam: PF00048; IL8; 1.
 DR SMART: SM00199; SCY; 1.
 DR PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
 DR Cytokine: Chemotaxis; Heparin-binding; Glycoprotein; Signal;
 KW Inflammatory response; 3d-structure.
 FT SIGNAL 1 23
 FT CHAIN 24 99
 FT MOD_RES 24 24
 FT DISULFID 34 59
 FT CARBOHYD 29 29
 FT CONFLICT 30 30
 FT CONFLICT 68 70
 FT SEQUENCE 99 AA; 11200 MW; 96048B371C25D00E CRC64;
 Query Match 59.4%; Score 337; DB 1; Length 99;
 Best Local Similarity 65.3%; Pred. No. 1.5e-30;
 Matches 64; Conservative 11; Mismatches 23; Indels 0; Gaps 0;
 Oy 11 MKVSALLCLLMATFSPGSLAOPDSVPTCCFVYINKRIPRLPRLSTRTINICP 70
 Db 1 MKASALLCLLTAAAFSPGSLAOPVGINSTPTCCYRINKRIPRRLSTRTINICP 60
 Oy 71 KEAVFTKRGKEVCADPKERVRDPMKHLDPFONLK 108
 Db 61 KEAVFTKRLKEICADPTQKWDPMKHLDKTQTPK 98
 RESULT 9
 SY13_HUMAN STANDARD; PRT; 98 AA.
 ID SY13_HUMAN
 AC Q99616; 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Small inducible cytokine A13 precursor (CC113) (Monocyte chemotactic
 DE protein 4) (MCP-4) (Monocyte chemoattractant protein 4) (CX-beta-10)
 DE (NCC-1).
 GN SCYA13 OR MCP4 OR NCC1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart.
 RX MEDLINE-97113354; PubMed-8955214;
 RA Garcia-Zepeda E.A., Combattiere C., Rothenberg M.E., Sarafi M.N.,
 RA Lavigne F., Hamid Q., Murphy P.M., Luster A.D.;
 RT "Human monocyte chemoattractant protein (MCP)-4 is a novel CC
 RT chemokine with activities on monocytes, eosinophils, and basophils
 RT induced in allergic and nonallergic inflammation that signals through
 RT the CC chemokine receptors (CCR)-2 and -3.";
 RL J. Immunol. 157:5613-5626(1996).
 RN [2]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 17-98.
 RC TISSUE=Fetal.
 RX MEDLINE-96235049; PubMed-8642349;
 RA Unguccioni M., Letscher P., Forssmann U., Dewald B., Li H., Lima S.H.,
 RA Li Y., Kreider B., Garcia G., Thelen M., Baggiolini M.;
 RT "Monocyte chemotactic protein 4 (MCP-4), a novel structural and
 RT functional analogue of MCP-3 and eotaxin.";
 RL J. Exp. Med. 183:2379-2384(1996).

[3]
 RN SEQUENCE FROM N.A., AND SEQUENCE OF 22-33.
 RP TISSUE-Petal;
 RC MEDLINE=97341179; PubMed=9195948;
 RA Berkhout T.A., Sarau H.M., Moores K., White J.R., Elshourbagy N.,
 RA Appelbaum E., Reape T.J., Brawner M., Makwana J., Foley J.J.,
 RA Schmidt D.B., Imbuglia C., Macnulty D., Matthews J., O'Donnell K.,
 RA O'Shannessy D., Scott M., Groot P.H.E., Macphae C.;
 RT "cloning, in vitro expression, and functional characterization of a
 RT novel human CC chemokine of the monocyte chemotactic protein (MCP)
 RT family (MCP-4) that binds and signals through the CC chemokine
 RT receptor 2B.";
 RL J. Biol. Chem. 272:16404-16413(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Dante M., Gibson A.;
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Lung;
 RA Power C.A., Meyer A., Rison S.C.G., Guye-Coulin F., Wells T.N.C.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97213770; PubMed=960459;
 RA Godiska R., Chantry D., Raport C.J., Schweickart V.L., Trong H.L.,
 RA Gray P.W.;
 RT "Monocyte chemotactic protein-4: tissue-specific expression and
 RT signaling through CC chemokine receptor-2.";
 RL J. Leukoc. Biol. 61:353-360(1997).
 RN [7]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Skin fibroblast;
 RX MEDLINE=9916086; PubMed=10049733;
 RA Hein H., Schluter C., Kulke R., Christophers E., Schroder J.M.,
 RA Bartsch J.;
 RT "Genomic organization, sequence analysis and transcriptional
 RT regulation of the human MCP-4 chemokine gene (SCYA13) in dermal
 RT fibroblasts: a comparison to other eosinophilic beta-chemokines.";
 RL Biochem. Biophys. Res. Commun. 255:470-476(1999).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RA Strausberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CHEMOTACTIC FACTOR THAT ATTRACTS MONOCYTES, LYMPHOCYTES,
 CC BASOPHILS AND EOSINOPHILS, BUT NOT NEUTROPHILS. SIGNALS THROUGH
 CC CCR2 AND CCR3 RECEPTORS. PLAYS A ROLE IN THE ACCUMULATION OF
 CC LEUKOCYTES AT BOTH SITES OF ALLERGIC AND NONALLERGIC INFLAMMATION.
 CC MAY BE INVOLVED IN THE RECRUITMENT OF MONOCYTES INTO THE ARTERIAL
 CC WALL DURING THE DISEASE PROCESS OF ARTERIOSCLEROSIS. MAY PLAY A
 CC ROLE IN THE MONOCYTE ATTRACTION IN TISSUES CHRONICALLY EXPOSED TO
 CC EXOGENOUS PATHOGENS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED. FOUND IN SMALL INTESTINE,
 CC THYMUS, COLON, LUNG, TRACHEA, STOMACH AND LYMPH NODE. LOW LEVELS
 CC SEEN IN THE PULMONARY ARTERY SMOOTH MUSCLE CELLS.
 CC -1- INDUCTION: BY INTERLEUKIN-1 AND TNF-ALPHA.
 CC -1- PFM: ONE MAJOR ISOFORM MCP-4, AND TWO MINOR ISOFORMS (LA)MCP-4 AND
 CC (FNPGLA)MCP-4 ARE PRODUCED BY DIFFERENTIAL SIGNAL CLEAVAGE.
 CC (LA)MCP-4 IS ABOUT 30 FOLD LESS ACTIVE THAN MCP-4.
 CC -1- MASS SPECTROMETRY: MM=9314; MW=ERR-30; METHOD-MALDI; RANGE=17-98.
 CC -1- MASS SPECTROMETRY: MM=8760; MW=ERR-30; METHOD-MALDI; RANGE=22-98.
 CC -1- MASS SPECTROMETRY: MM=8575; MW=ERR-30; METHOD-MALDI; RANGE=24-98.
 CC -1- MISCELLANEOUS: THIS PROTEIN CAN BIND HEPARIN.
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
 CC C-C) (CHEMOKINE CC).
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U46767; AAB38703.1; -
 DR EMBL: AC002482; AAB67307.1; -
 DR EMBL: X98306; CAA66950.1; -
 DR EMBL: U59808; AAD09362.1; -
 DR EMBL: AJ001634; CAA04888.1; -
 DR EMBL: BC008621; AAH08621.1; -
 DR HSSP: P51671; 1EOT.
 DR GeneW: HGNC:10611; SCYA13.
 DR MIM: 601391; -
 DR InterPro: IPR000827; CC-Chemokine-sm1.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR Pfam: PF00048; IL8; 1.
 DR SMART: SM00199; SCY; 1.
 DR PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
 DR CYTOKINE: Chemotaxis; Signal; Glycoprotein; Inflammatory response.
 KW SIGNAL 1 16 SMALL INDUCIBLE CYTOKINE A13, LONG FORM.
 FT CHAIN 17 98 SMALL INDUCIBLE CYTOKINE A13, SHORT FORM.
 FT CHAIN 24 98 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 24 24 BY SIMILARITY.
 FT DISULFID 34 58
 FT DISULFID 35 74
 FT CARBOHYD 29 29 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 98 AA; 10986 MW; 612688DECD308873 CRC64;
 Query Match 57.9%; Score 328.5; DB 1; Length 98;
 Best Local Similarity 62.2%; Pred. No. 1,3e-29;
 Matches 61; Conservative 18; Mismatches 18; Indels 1; Gaps 1;
 Oy 11 MVSAAALCLLLMAATFSPQGLAOPDSVSIPTCCFNVINRKIPRIRESYPTITNOCF 70
 Db 1 MVSASVLLCLLLMTAFNFGAQPDPALVNPSTCFESSKSLISLRLSYV-ITTSRCP 59
 Oy 71 KEAVIFKTRGKREKVCADPKERVRDMSKHLDPFONLK 108
 Db 60 OKAVIFKTRGKREKVCADPKERVRDMSKHLDPFONLK 97
 RESULT 10
 SY02_CANFA
 ID SY02_CANFA STANDARD; PRT; 101 AA.
 AC P52203.
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemotactic
 DE protein 1) (MCP-1) (Monocyte chemoattractant protein-1).
 GN SCYA2 OR MCP1.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-jugular vein endothelial;
 RX MEDLINE=971176620; PubMed=9024159;
 RA Kumar A.G., Ballantyne C.M., Michael L.H., Kukiela G.L., Youker K.A.,
 RA Lindsey M.L., Hawkins H.K., Birdsall H.H., Mackey C.R., Larosa G.J.,
 RA Rossen R.D., Smith C.W., Entman M.L.;
 RT "Induction of monocyte chemoattractant protein-1 in the small veins
 RT of the ischemic and reperused canine myocardium.";
 RL Circulation 95:693-700(1997).
 CC -1- FUNCTION: CHEMOTACTIC FACTOR THAT ATTRACTS MONOCYTES, BUT NOT
 CC NEUTROPHILS. IMPORTANT FACTOR IN THE COURSE OF THE INFLAMMATORY
 CC REACTION TO REPERUSION OF THE PREVIOUSLY ISCHEMIC MYOCARDIUM.
 CC MAY PLAY A SIGNIFICANT ROLE IN MONOCYTE TRAFFICKING INTO THE
 CC REPERUSED MYOCARDIUM.
 CC -1- SUBUNIT: MONOMER OR HOMODIMER; IN EQUILIBRIUM (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: ENDOTHELIUM OF SMALL VEINS AND INTRAVASCULAR
 CC VEINS, AND INFILTRATING LEUKOCYTES.

```

CC -1- INDUCTION: BY TNF-ALPHA.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: 029653; AA04911.1; -.
CC HSSP: P13500; IDOM.
CC InterPro: IPR000827; CC_chemkine_sml.
CC InterPro: IPR001811; Chemokine_IL8.
CC Pfam: PF00048; IL8; 1.
CC SMART: SM00199; SCV; 1.
CC PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
CC Cytokine; Chemotaxis; Signal; Inflammatory response.
CC SIGNAL 1 23
CC CHAIN 24 101
CC MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID (BY
CC SIMILARITY).
CC DISULFID 34 59
CC DISULFID 35 75 BY SIMILARITY.
CC SEQUENCE 101 AA; 11121 MW; CDDYE2B1901A7267 CRC64;

Query Match 57.7%; Score 327; DB 1; Length 101;
Best Local Similarity 64.1%; Pred. No. 1.9e-29;
Matches 59; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

QY 11 MKVSALLCLLIMATFSPGLOAPDSVSIPITCCFNVINKRIPORLESTRITNIQCP 70
DB 1 MKVSALLCLLILAAATITQVLTPDPAISPVTCYTLTKNKISIQRLASKRYTSSQCP 60
QY 71 KEAVIFKTRKEVCADPKERWVRDSKMLDQ 102
DB 61 KEAVIFKTVLNKEICADPKKQWDSMAHLDK 92

RESULT 11
SY12_MOUSE STANDARD; PRT; 104 AA.
AC 062401; 09OYD6;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Small inducible cytokine A12 precursor (CCIL12) (Monocyte chemotactic
DE protein 5) (MCP-5) (MCP-1 related chemokine).
GN SCYA12 OR MCP5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=9709149; PubMed=8920881;
RA Jia G.-O., Gonzalez J.A., Lloyd C., Kremer L., Lu L., Martinez A.C.,
RA Wershall B.R., Gutierrez-Ramos J.C.;
RA "Distinct expression and function of the novel mouse chemokine
RT monocyte chemotactic protein-5 in lung allergic inflammation.";
RL J. Exp. Med. 184:1939-1951(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97149438; PubMed=8996246;
RX Sarafi M.N., Garcia-Zepeda E.A., McLean J.A., Charo I.F., Luster A.D.;
RT "Murine monocyte chemoattractant protein (MCP)-5: a novel CC
RT chemokine that is a structural and functional homologue of human
RT MCP-1."
RL J. Exp. Med. 185:99-109(1997).
RN [3]
RP SEQUENCE FROM N.A.

```

```

RC STRAIN-B10 S/J, BALB/C, DBA/2J, NOD/LtJ, and SJL/J; TISSUE=Spleen;
RX MEDLINE=99370037; PubMed=10438970;
RA Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,
RA Blankenhorn E.P.;
RT "Sequence polymorphisms in the chemokines SCYA1 (TCA-3), SCYA2
RT (monocyte chemoattractant protein (MCP)-1), and SCYA12 (MCP-5) are
RT candidates for eae7, a locus controlling susceptibility to monophasic
RT remitting/nonrelapsing experimental allergic encephalomyelitis.";
RL J. Immunol. 163:2262-2266(1999).
CC -1- FUNCTION: CHEMOTACTIC FACTOR THAT ATTRACTS EOSINOPHILS, MONOCYTES,
CC AND LYMPHOCYTES BUT NOT NEUTROPHILS. POTENT MONOCYTE ACTIVE
CC CHEMOKINE THAT SIGNALS THROUGH CCR2. INVOLVED IN ALLERGIC
CC INFLAMMATION AND THE HOST RESPONSE TO PATHOGENS AND MAY PLAY A
CC PIVOTAL ROLE DURING EARLY STAGES OF ALLERGIC LONG INFLAMMATION.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE LYMPH NODES AND
CC THYMUS. ALSO FOUND IN THE SALIVARY GLANDS CONTAINING LYMPH NODES,
CC BREAST, HEART, LUNG, BRAIN, SMALL INTESTINE, KIDNEY AND COLON.
CC -1- INDUCTION: BY INTERFERON GAMMA AND LIPOLYSACCHARIDE (LPS).
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U50712; AAB50053.1; -.
CC EMBL: U6670; AAB49424.1; -.
CC EMBL: AF065934; AAF15384.1; -.
CC EMBL: AF065935; AAF15385.1; -.
CC EMBL: AF065936; AAF15386.1; -.
CC EMBL: AF065937; AAF15387.1; -.
CC EMBL: AF065938; AAF15388.1; -.
CC HSSP: P13500; IDOL.
CC MGD: MGI:108224; Scya12.
CC InterPro: IPR000827; CC_chemkine_sml.
CC InterPro: IPR001811; Chemokine_IL8.
CC Pfam: PF00048; IL8; 1.
CC SMART: SM00199; SCV; 1.
CC PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
CC Cytokine; Chemotaxis; Signal; Inflammatory response.
CC SIGNAL 1 22
CC CHAIN 23 104
CC DISULFID 33 58
CC DISULFID 34 74 BY SIMILARITY.
CC VARIANT 94 104 OTFLEPCIG -> RT (IN STRAIN SJL/J).
CC SEQUENCE 104 AA; 11659 MW; 8D1024F4CC3DBF CRC64;

Query Match 56.3%; Score 319.5; DB 1; Length 104;
Best Local Similarity 59.4%; Pred. No. 1.3e-28;
Matches 60; Conservative 21; Mismatches 17; Indels 3; Gaps 2;

QY 11 MKVSALLCLLIMATFSPGLOAPDSVSIPITCCFNVINKRIPORLESTRITNIQCP 70
DB 1 MKIS-TLLCLLIATITSPVLAGDAVSTPVCYVWVKQIHVRKLSYRRITSSQCP 59
QY 71 KEAVIFKTRKEVCADPKERWVRDSKMLDQIFON-LKP 109
DB 60 KEAVIFKTRIDKEICADPKERWVRDSKMLDQIFON-LKP 100

RESULT 12
MCPA_BOVIN STANDARD; PRT; 99 AA.
ID MCPA_BOVIN
AC P28291;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)

```


DE Monocyte chemotactic protein 1A precursor (MCP-1A) (MCP-1) (Acidic
DE seminal fluid protein).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Seminal plasma;
RX MEDLINE=92096117; PubMed=1721821;
RA Wempe F., Henschen A., Scheit K.H.;
RT "Gene expression and cDNA cloning identified a major basic protein
RT constituent of bovine seminal plasma as bovine
RT monocyte-chemoattractant protein-1 (MCP-1).";
RL DNA Cell Biol. 10:671-679(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Seminal plasma;
RX MEDLINE=92181448; PubMed=1543494;
RA Wempe F., Einspanier R., Scheit K.H.;
RT "Characterization by cDNA cloning of the mRNA of a new growth factor
RT from bovine seminal plasma: acidic seminal fluid protein.";
RL Biochem. Biophys. Res. Commun. 183:232-237(1992).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=94338337; PubMed=8060303;
RA Wempe F., Kuhlmann J.K., Scheit K.H.;
RT "Characterization of the bovine monocyte chemoattractant protein-1
RT gene";
RL Biochem. Biophys. Res. Commun. 202:1272-1279(1994).
CC -1- FUNCTION: CHEMOTACTIC FACTOR THAT ATTRACTS MONOCYTES, BUT NOT
CC NEUTROPHILS.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; L32659; AAA60956.1; -;
CC EMBL; M84602; AAA30651.1; -;
CC PIR; A39296; A39296.
CC PIR; JC2336; JC2336.
CC HSSP; P13500; IDOM.
CC InterPro; IPR000827; CC_Chemkine_sml.
CC InterPro; IPR001811; Chemokine_IL8.
CC SMART; SM00199; SCY; 1.
CC PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
CC CYTOKINE; Chemotaxis; Signal.
CC SIGNAL 1 23 BY SIMILARITY.
CC CHAIN 24 99 MONOCYTE CHEMOTACTIC PROTEIN 1A.
CC MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID (BY
CC SIMILARITY).
CC DISULFID 34 59 BY SIMILARITY.
CC DISULFID 35 75 BY SIMILARITY.
CC SEQUENCE 99 AA; 1114 MW; 0FD79FCLABOCBE88 CRC64;
Query Match 53.3%; Score 302; DB 1; Length 99;
Best Local Similarity 56.6%; Pred. No. 1; le-26;
Matches 56; Conservative 21; Mismatches 22; Indels 0; Gaps 0;
QY 11 MKVSAALLCLLLMAATFSPQGLAQPDSVSIPTCCFNVINRKIPDIORLESYTRITNIQCP 70
DB 1 MKVSAALLCLLLTVAFAFSSHYLAQPDVNSPVCCYFTKTIKTVSRKLMYSRRINSTKCP 60
QY 71 KEAVIFKTRKGEVCADPKERWVRDSMKHLDQIFONLKP 109
||||| |||:|||||:||||:|:|:|

DB 61 KEAVIFKTLILGKELCADPKOKWVQDSINILNKKNTPKP 99
RESULT 13
ST02_RABIT STANDARD; PRT; 125 AA.
ID SY02_RABIT
AC P28292;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemotactic
DE protein 1) (MCP-1) (Monocyte chemoattractant protein-1).
GN SCY2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-New Zealand white; TISSUE-spleen;
RX MEDLINE=91225489; PubMed=2026877;
RA Yoshimura T., Yunkai N.;
RT "Neutrophil attractant/activation protein-1 and monocyte
RT chemoattractant protein-1 in rabbit. cDNA cloning and their
RT expression in spleen cells.";
RL J. Immunol. 146:3483-3488(1991).
CC -1- FUNCTION: CHEMOTACTIC FACTOR THAT ATTRACTS MONOCYTES, BUT NOT
CC NEUTROPHILS.
CC -1- SUBUNIT: MONOMER OR HOMODIMER; IN EQUILIBRIUM (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; M57440; AAA11386.1; -;
CC HSSP; P13500; IDOM.
CC InterPro; IPR000827; CC_Chemkine_sml.
CC InterPro; IPR001811; Chemokine_IL8.
CC SMART; PF00048; IL8; 1.
CC SMART; SM00199; SCY; 1.
CC PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
CC CYTOKINE; Chemotaxis; Signal; Inflammatory response; Glycoprotein.
CC SIGNAL 1 23 BY SIMILARITY.
CC CHAIN 24 125 SMALL INDUCIBLE CYTOKINE A2.
CC MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID (BY
CC SIMILARITY).
CC DISULFID 34 59 BY SIMILARITY.
CC DISULFID 35 75 BY SIMILARITY.
CC CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 125 AA; 13776 MW; 24C3A542CB6A47EE CRC64;
Query Match 52.6%; Score 298; DB 1; Length 125;
Best Local Similarity 56.1%; Pred. No. 4e-26;
Matches 55; Conservative 18; Mismatches 25; Indels 0; Gaps 0;
QY 11 MKVSAALLCLLLMAATFSPQGLAQPDSVSIPTCCFNVINRKIPDIORLESYTRITNIQCP 70
DB 1 MKVSAALLCLLLTVAFAFSSHYLAQPDVNSPVCCYFTKTIKTVSRKLMYSRRINSTKCP 60
QY 71 KEAVIFKTRKGEVCADPKERWVRDSMKHLDQIFONLKP 108
DB 61 KEAVIFKTLILGKELCADPKOKWVQDSINILNKKNTPKP 98
||||| |||:|||||:||||:|:|:|

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2003, 02:02:16 ; Search time 81 Seconds
(without alignments)
277.273 Million cell updates/sec

Title: US-10-033-067-1

Perfect score: 567
Sequence: 1 MKLTPRPSKMKVSAALLCL.....ERWVRDSMKHLDQIFQNLKP 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SEPREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_humani:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	359	63.3	100	6 095MD5	095MD5 bos taurus
2	321	56.6	99	6 09TRQ3	09TRQ3 equus caball
3	315	55.6	100	6 09TRQ4	09TRQ4 equus caball
4	313	55.2	81	6 09TRQ2	09TRQ2 equus caball
5	287	50.6	97	6 09TRQ6	09TRQ6 bos taurus
6	281	49.6	97	11 092318	092318 cavia porce
7	264.5	46.6	79	4 095689	095689 homo sapien
8	259.5	45.8	75	6 09TRQ1	09TRQ1 equus caball
9	259	45.7	148	11 09QYD7	09QYD7 mus musculu
10	185.5	32.7	90	13 09PWA6	09PWA6 gallus gall
11	185.5	32.7	90	13 091OC9	091OC9 gallus gall
12	183.5	32.4	93	4 096T68	096T68 homo sapien
13	179	31.6	44	6 09B683	09B683 pongo pygma
14	177.5	31.3	92	11 0912L0	0912L0 sigmodon hl
15	173	30.5	62	4 095690	095690 homo sapien
16	170	30.0	106	11 092292	092292 cricetus

17	169.5	29.9	93	6 08SQA6	08SQA6 bos taurus
18	169	29.8	91	11 0912L1	0912L1 sigmodon hl
19	166.5	29.4	91	13 08Q657	08Q657 gallus gall
20	162	28.6	92	6 08SQ40	08SQ40 felis silve
21	161	28.4	80	4 014745	014745 homo sapien
22	160	28.2	92	11 091265	091265 sigmodon hl
23	156	27.5	91	13 08Q656	08Q656 gallus gall
24	154.5	27.2	93	11 09ERQ0	09ERQ0 rattus norv
25	151	26.6	89	13 0918E0	0918E0 gallus gall
26	145.5	25.7	95	12 098158	098158 kaposi's sa
27	143.5	25.3	99	6 095N01	095N01 canis famil
28	133	23.5	93	11 09WU26	09WU26 mus musculu
29	133	23.5	121	11 09R043	09R043 mus musculu
30	130.5	23.0	100	13 08Q655	08Q655 gallus gall
31	128	22.6	395	11 091V44	091V44 mus musculu
32	119.5	21.1	97	6 09BD22	09BD22 bos taurus
33	116	20.5	97	13 057411	057411 gallus gall
34	112.5	19.8	76	11 09QUR9	09QUR9 mus musculu
35	108.5	19.1	96	6 08SQB1	08SQB1 bos taurus
36	108	19.0	133	11 091V84	091V84 mus musculu
37	107.5	19.0	100	13 09PT05	09PT05 oncorhynch
38	107	18.9	92	11 09QZU2	09QZU2 mus musculu
39	105.5	18.6	76	11 09QUS5	09QUS5 mus musculu
40	105	18.5	92	11 091Z85	091Z85 rattus norv
41	104.5	18.4	101	13 093238	093238 cyprinus ca
42	103.5	18.3	100	13 09PT07	09PT07 oncorhynch
43	103.5	18.3	100	13 09PT06	09PT06 oncorhynch
44	103.5	18.3	100	13 09PT03	09PT03 oncorhynch
45	103.5	18.3	100	13 09W691	09W691 oncorhynch

ALIGNMENTS

RESULT 1

ID	Q95MD5	PRELIMINARY;	PRT;	100 AA.
AC	Q95MD5;			
DT	01-DEC-2001 (TREMBLrel, 19, Created)			
DT	01-DEC-2001 (TREMBLrel, 19, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel, 20, Last annotation update)			
DE	Chemottractant protein 2 (Fragment).			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_Taxid=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Wierling D.;			
RT	"Role of chemokines in respiratory syncytial virus infection."			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF399641; AAK94451.1;			
DR	InterPro; IPR000827; CC_Chemkine_sml.			
DR	InterPro; IPR001811; Chemokine_IL8.			
DR	Pfam; PF00048; IL8; 1.			
DR	PROSITE; PS00472; SMALL_CYTOKINES_CC; UNKNOWN_1.			
FT	NON_TER			
SQ	SEQUENCE 100 AA; 11001 MW; F1D308AD924FCAR6 CRC64;			
Query Match	63.3%; Score 359; DB 6; Length 100;			
Best local Similarity	68.7%; Pred. No. 6.4e-34;			
Matches	68; Conservative 15; Mismatches 16; Indels 0; Gaps 0;			
QY	11 MKVSAAALCLLMAATSPGGLAOPDSVSIPTCCFNINRKPIQLRLESTRITNIOCP 70			08SQA6 bos taurus
DB	2 MKVSAGIICLLVATFETGVLAQPDVSPTTCFVSINGKIPKIDSYRTINSOCP 61			0912L1 sigmodon hl
QY	71 KEAVIFKTRKGEKVCADPKERWVRDSMKHLDQIFQNLKP 109			08Q657 gallus gall
DB	62 QEAVIFKTRKADVDYCADPKERWVRDSMKHLDQIFQNLKP 100			08SQ40 felis silve

RESULT 2

ID 09TT03 PRELIMINARY; PRT; 99 AA.
 AC 09TT03;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Monocyte chemoattractant protein-1 precursor.
 GN MCP-1.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LUNG;
 RX MEDLINE=21061912; PubMed=11044560;
 RA Benarafa C., Cunningham F.M., Hamblin A.S., Horohov D.W.,
 RA Collins M.E.;
 RT "Cloning of equine chemokines eotaxin, monocyte chemoattractant
 RT protein (MCP)-1, MCP-2 and MCP-4, mRNA expression in tissues and
 RT induction by IL-4 in dermal fibroblasts."
 RL Vet. Immunol. Immunopathol. 76:283-298(2000).
 DR HSSP; P13500; IDOM.
 DR InterPro: IPR000827; CC_Chemokine_sml.
 DR Pfam: PF00048; IL6; 1.
 DR SMART; SM00199; SCY; 1.
 DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
 KW Signal.
 FT CHAIN 1 23 POTENTIAL.
 FT SIGNAL 24 99 MONOCYTE CHEMOATTRACTANT PROTEIN-1.
 SQ SEQUENCE 99 AA; 10790 MM; BA1448F79F3423D2 CRC64;

Query Match 56.6%; Score 321; DB 6; Length 99;
 Best Local Similarity 60.6%; Pred. No. 1.6e-29;
 Matches 60; Conservative 17; Mismatches 22; Indels 0; Gaps 0;

QY 11 MKVSALLCLLMAATFSPGGLAOPDSVSIPTCCFNVINRKIPRIQRLSYRTITNIQCP 70
 DB 1 MKVSALLCLLTLTAATFSTVLAQPDAINSPVTCYFTGKISSRLGSKVTSKCP 60
 QY 71 KEAVIFKTRKRGKVCADPKERWRDSMKHLDOIIFQNLKP 109
 DB 61 KEAVIFKTRKRGKVCADPKERWRDSMKHLDOIIFQNLKP 99
 RESULT 3
 ID 09TT04 PRELIMINARY; PRT; 100 AA.
 AC 09TT04;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Eotaxin precursor.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21061912; PubMed=11044560;
 RA Benarafa C., Cunningham F.M., Hamblin A.S., Horohov D.W.,
 RA Collins M.E.;
 RT "Cloning of equine chemokines eotaxin, monocyte chemoattractant
 RT protein (MCP)-1, MCP-2 and MCP-4, mRNA expression in tissues and
 RT induction by IL-4 in dermal fibroblasts."
 RL Vet. Immunol. Immunopathol. 76:283-298(2000).
 DR HSSP; A251188; CAB61624.1;
 DR SMART; P51671; LEOT.
 DR InterPro: IPR000827; CC_Chemokine_sml.
 DR InterPro: IPR001811; Chemokine_IL6.

DR Pfam; PF00048; IL6; 1.
 DR SMART; SM00199; SCY; 1.
 DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
 KW Signal.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 100 EOTAXIN.
 SQ SEQUENCE 100 AA; 11247 MM; 11F08BC00E75D508 CRC64;

Query Match 55.6%; Score 315; DB 6; Length 100;
 Best Local Similarity 65.2%; Pred. No. 7.9e-29;
 Matches 60; Conservative 16; Mismatches 14; Indels 2; Gaps 1;

QY 11 MKVSALLCLLMAATFSPGGLAOPDSVSIPTCCFNVINRKIPRIQRLSYRTITNIQCP 70
 DB 1 MKVSALLCLLTLTAATFSTVLAQPD--VSIIVCCFNVNASKRISFORLSYRTITSSKCP 58
 QY 71 KEAVIFKTRKRGKVCADPKERWRDSMKHLDO 102
 DB 59 QKAVIFKTRKAKKICADPKRKQWQDAMKYLDE 90

RESULT 4

ID 09TT02 PRELIMINARY; PRT; 81 AA.
 AC 09TT02;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Monocyte chemoattractant protein-2 precursor (Fragment).
 GN MCP-2.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LUNG;
 RX MEDLINE=21061912; PubMed=11044560;
 RA Benarafa C., Cunningham F.M., Hamblin A.S., Horohov D.W.,
 RA Collins M.E.;
 RT "Cloning of equine chemokines eotaxin, monocyte chemoattractant
 RT protein (MCP)-1, MCP-2 and MCP-4, mRNA expression in tissues and
 RT induction by IL-4 in dermal fibroblasts."
 RL Vet. Immunol. Immunopathol. 76:283-298(2000).
 DR EMBL; A251190; CAB61626.1;
 DR HSSP; P13500; IDOK.
 DR InterPro: IPR001811; Chemokine_IL6.
 DR Pfam; PF00048; IL6; 1.
 DR SMART; SM00199; SCY; 1.
 KW Signal.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 >81 BY SIMILARITY.
 FT NON_TER 81
 SQ SEQUENCE 81 AA; 8858 MM; A34ADE103C386B0F CRC64;

Query Match 55.2%; Score 313; DB 6; Length 81;
 Best Local Similarity 72.8%; Pred. No. 1.1e-28;
 Matches 59; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 11 MKVSALLCLLMAATFSPGGLAOPDSVSIPTCCFNVINRKIPRIQRLSYRTITNIQCP 70
 DB 1 MKVSALLCLLTLTAATFSTVLAQPDVAIVPTCCFNVNASKRISFORLSYRTITSSKCP 60
 QY 71 KEAVIFKTRKRGKVCADPKER 91
 DB 61 QEAVIFKTRKRGKVCADPKER 81

RESULT 5

ID 09TT06 PRELIMINARY; PRT; 97 AA.
 AC 09TT06;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)

```
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE Botaxin.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Vogel B., Klinder A., Aust G.;
RT "Molecular cloning of bovine eotaxin mRNA.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ132003; CAB61617.1; -.
DR HSSP; P51671; 1EOT.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
SQ SEQUENCE 97 AA; 10965 MW; 9E65F23E1DDEB743 CRC64;

Query Match
Best Local Similarity 50.6%; Score 287; DB 6; Length 97;
Matches 56; Conservative 19; Mismatches 21; Indels 2; Gaps 1;

QY 11 MKVSALLCLLMAATFSPGGLAOPDSVSIPTCCFNVNKRKIPQRLSTRTITNIQCP 70
DB 1 MKVSALLCLLTAATFSLTCSIQVLAOP--ASIPITCCFNMNSKKSISQRLSYRKITSSKCP 58
QY 71 KEAVIFTKRGKEVCADPKERWVDSMKHLDQIFQNK 108
DB 59 OKAVIFTKRGKRCVDPQKRWONAMEYLNOKSQTLEK 96

RESULT 6
Q92318 PRELIMINARY; PRT; 97 AA.
AC Q92318;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Monocyte chemoattractant protein-3 (MCP-3).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=LUNG;
RA Asano K., Nakamura M., Oguma T., Fukunaga K., Matsubara H.,
RA Ishizaka A., Yamaguchi K., Kanazawa M.;
RT "Differential expression of CC chemokines in guinea pig lungs during
RT an allergic inflammation.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB014340; BAA36456.1; -.
DR HSSP; P51671; 1EOT.
DR InterPro: IPR000827; CC_chemkine_sml.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 97 AA; 11159 MW; E1B9A17C165C2421 CRC64;

Query Match
Best Local Similarity 49.6%; Score 281; DB 11; Length 97;
Matches 56; Conservative 18; Mismatches 16; Indels 2; Gaps 2;

QY 11 MKVSALLCLLMAATFSPGGLAOPDSVSIPTCCFNVNKRKIPQRLSTRTITNIQCP 70
DB 1 MOVIANVLLCLLTAANFSSLLAOPDSGVNIS-ITCYA-RSQRINVRLESTRTITSSKCP 58
QY 71 KEAVIFTKRGKEVCADPKERWVDSMKHLDQ 102
DB 59 WQAVIFTKRNRRLCADPKQKQWQDSMKYIDK 90
```

```
RESULT 7
Q95689 PRELIMINARY; PRT; 79 AA.
AC Q95689;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE CC-chemokine (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=FORESKIN;
RA Bartels J.H., Schlueter C., Richter E., Noso N., Christophers E.,
RA Schroeder J.M.;
RT "Expression of a MCP-4 like novel CC-chemokine in human dermal
RT fibroblasts: molecular cloning and RT-PCR analysis.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z77650; CAB01111.1; -.
DR HSSP; P51671; 1EOT.
DR InterPro: IPR000827; CC_chemkine_sml.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
FT NON_TER 1
SQ SEQUENCE 79 AA; 8987 MW; 4FCF42983D46C352 CRC64;

Query Match
Best Local Similarity 46.2%; Score 264.5; DB 4; Length 79;
Matches 46; Conservative 17; Mismatches 10; Indels 1; Gaps 1;

QY 27 FSPQGLAOPDSVSIPTCCFNVNKRKIPQRLSTRTITNIQCPKEAVIFTKRGKEVCA 86
DB 1 FNPQGLAOPDALNVSTCCFFSSKKSISQRLKSYV-ITTSRCPQKAVIFPRKLGKEICA 59
QY 87 DPKERWVDSMKHL 100
DB 60 DPKERWVQNMKHL 73

RESULT 8
Q9TTQ1 PRELIMINARY; PRT; 75 AA.
AC Q9TTQ1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE Monocyte chemoattractant protein-4 precursor (Fragment).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21061912; PubMed=11044560;
RA Benarafa C., Cunningham F.M., Hamblin A.S., Horohov D.W.,
RA Collins M.E.;
RT "Cloning of equine chemokines eotaxin, monocyte chemoattractant
RT protein (MCP)-1, MCP-2 and MCP-4, mRNA expression in tissues and
RT induction by IL-4 in dermal fibroblasts.";
RL Vet. Immunol. Immunopathol. 76:283-298(2000).
DR EMBL; AJ251191; CAB61627.1; -.
DR HSSP; P51671; 1EOT.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
KW signal.
```

FT NON_TER 1 1
 FT SIGNAL <1 18 POTENTIAL.
 FT CHAIN 19 >75 MONOCYTE CHEMOATTRACTANT PROTEIN-4.
 FT NON_TER 75 75
 FT SEQUENCE 75 AA; 827 MW; 480A5267AC6A03E5 CRC64;

Query Match
 Best Local Similarity 45.8%; Score 259.5; DB 6; Length 75;
 Matches 50; Conservative 11; Mismatches 14; Indels 1; Gaps 1;

QY 16 ALICLLLMATSPGGLAOPDSVSIPTCCFVNINRKIPQRLSEYTRITNIQCPKEAVI 75
 DB 1 ALICLLLMATSPGGLAOPDSVSIPTCCFVNINRKIPQRLSEYTRITNIQCPKEAVI 59
 QY 76 FTKRKGRKVCADPKER 91
 DB 60 FTKRKGRKVCADPKER 75

RESULT 9
 Q9QYD7 PRELIMINARY; PRT; 148 AA.

AC Q9QYD7
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Small inducible cytokine A2.
 GN SCYA2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ST/J; TISSUE=SPLEEN;
 RX MEDLINE-99370037; PubMed-10438970;
 RA Teuscher C., Butterfield R.D., Ma R.Z., Zachary J.F., Doege R.W.,
 RA Blankenhorn E.P.;
 RT "Sequence polymorphisms in the chemokines SCYA1 (TCA-3), SCYA2
 RT (monocyte chemoattractant protein (MCP)-1), and SCYA12 (MCP-5) are
 RT candidates for eae7, a locus controlling susceptibility to monophasic
 RT remitting/nonrelapsing experimental allergic encephalomyelitis";
 RL J. Immunol. 163:2262-2266(1999).
 DR EMBL; AF065929; AAF15379.1; -;
 DR HSSP; P13500; 1DOK.
 DR MGD; MGI:98259; SCYA2.
 DR InterPro: IPR000827; CC_Chemkine_sml.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR Pfam; PF00048; IL8; 1.
 DR SMART; SM00199; SCY; 1.
 DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
 DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
 SQ SEQUENCE 148 AA; 16268 MW; 2BA24C5D19C489EB CRC64;

Query Match
 Best Local Similarity 45.7%; Score 259; DB 11; Length 148;
 Matches 49; Conservative 18; Mismatches 25; Indels 0; Gaps 0;

QY 11 MKVSALLCLLMAATSPGGLAOPDSVSIPTCCFVNINRKIPQRLSEYTRITNIQCP 70
 DB 1 MKVSALLCLLMAATSPGGLAOPDSVSIPTCCFVNINRKIPQRLSEYTRITNIQCP 60
 QY 71 KEAVIFTKRKGRKVCADPKERWVRDSMKHLD 102
 DB 61 KEAVIFTKRKGRKVCADPKERWVRDSMKHLD 92

RESULT 10
 Q9PWA6 PRELIMINARY; PRT; 90 AA.
 AC Q9PWA6
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)

DE Chemokine.
 GN SCYA4.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hughes S.M., Bumstead N.;
 RT "Mapping of the gene encoding the chicken homologue of the mammalian
 RT chemokine SCYA4."
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF146730; AAD48772.1; -;
 DR HSSP; P13236; 1HUM.
 DR InterPro: IPR000827; CC_Chemkine_sml.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR Pfam; PF00048; IL8; 1.
 DR SMART; SM00199; SCY; 1.
 DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
 DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
 SQ SEQUENCE 90 AA; 9986 MW; 50AF9679A26751CB CRC64;

Query Match
 Best Local Similarity 41.8%; Score 185.5; DB 13; Length 90;
 Matches 38; Conservative 17; Mismatches 33; Indels 3; Gaps 2;
 QY 11 MKVSALLCLLMAATSPGGLAOPDSVSIPTCCFVNINRKIPQRLSEYTRITNIQCP 70
 DB 1 MKVSALLCLLMAATSPGGLAOPDSVSIPTCCFVNINRKIPQRLSEYTRITNIQCP 57
 QY 71 KEAVIFTKRKGRKVCADPKERWVRDSMKHLD 101
 DB 58 HAGVIFTRKGRKVCANPDNDVDMYNNKME 88

RESULT 11
 Q910C9 PRELIMINARY; PRT; 90 AA.
 AC Q910C9
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Macrophage inflammatory protein 1-beta.
 GN SCYA4.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hughes S.M., Bumstead N.;
 RT "Mapping of the gene encoding the chicken homologue of the mammalian
 RT chemokine SCYA4."
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ243034; CAB45103.1; -;
 DR InterPro: IPR000827; CC_Chemkine_sml.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR Pfam; PF00048; IL8; 1.
 DR PROSITE; PS00472; SMALL_CYTOKINES_CC; UNKNOWN.1.
 DR PROSITE; PS00472; SMALL_CYTOKINES_CC; UNKNOWN.1.
 SQ SEQUENCE 90 AA; 9987 MW; 50AF9679A267408F CRC64;

Query Match
 Best Local Similarity 41.8%; Score 185.5; DB 13; Length 90;
 Matches 38; Conservative 17; Mismatches 33; Indels 3; Gaps 2;
 QY 11 MKVSALLCLLMAATSPGGLAOPDSVSIPTCCFVNINRKIPQRLSEYTRITNIQCP 70
 DB 1 MKVSALLCLLMAATSPGGLAOPDSVSIPTCCFVNINRKIPQRLSEYTRITNIQCP 57
 QY 71 KEAVIFTKRKGRKVCADPKERWVRDSMKHLD 101
 DB 58 HAGVIFTRKGRKVCANPDNDVDMYNNKME 88

```
RESULT 12
ID 096168 PRELIMINARY: PRT; 93 AA.
AC 096168;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Similar to small inducible cytokine A3 (homologous to mouse
Mip-1a).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-CELL;
RA Strassberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC007783; AAH07783.1;
DR InterPro: IPR000827; CC_ChemKine_sml.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR PROSITE: PS00472; SMALL_CYTOKINES_CC; UNKNOWN_1.
SQ SEQUENCE 93 AA; 10144 MW; A7A8E374006D61E CRC64;

Query Match
Best Local Similarity 41.8%; Score 183.5; DB 4; Length 93;
Matches 38; Conservative 15; Mismatches 37; Indels 1; Gaps 1;

OY 11 MKVSAALLCLLMATFSPQGLAOPDSVSIPTCCFNVINKRIPQRLSYTRITNIQCP 70
DB 1 MOVSTALAVLCTMALCQVLSAPLADPTACFSYTSRQIPQNIADYFE-TSSQCS 59
OY 71 KEAVIFKTRKGEVCADPKERWRDMSKHL 101
DB 60 KPSVIFLTRKRGVCAADPSEEWQKYVSLE 90

RESULT 13
ID 09B683 PRELIMINARY: PRT; 44 AA.
AC 09B683;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Monocyte chemotactic protein 1 (Fragment).
GN MCP1.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Ayi T.C., Chew X.L.A., Yap P.H.E.;
RL "Comparison between human and primate genomes.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF324469; AAK13442.1;
DR HSSP: P13500; IDOK.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 44 AA; 4830 MW; 1DE3C10EB83CD190 CRC64;

Query Match
Best Local Similarity 72.1%; Score 179; DB 6; Length 44;
Matches 31; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

OY 19 CLLMATFSPQGLAOPDSVSIPTCCFNVINKRIPQRLSY 61
DB 1 CLLMATFSPQGLAOPDAINAVTCYNTNKTISQVRLASY 43
```

```
RESULT 14
ID 0912L0 PRELIMINARY: PRT; 92 AA.
AC 0912L0;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Macrophage inflammatory protein 1 beta.
GN MIP-1BETA.
OS Sigmodon hispidus (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Sigmodon.
OX NCBI_TaxID=42415;
RN [1]
RP SEQUENCE FROM N.A.
RA Bianco J.C., Pletneva L.M., Prince G.A.;
RT "Sigmodon hispidus cytokines, chemokines and interferons.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF421392; AAL16933.1;
DR InterPro: IPR000827; CC_ChemKine_sml.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR PROSITE: PS00472; SMALL_CYTOKINES_CC; UNKNOWN_1.
SQ SEQUENCE 92 AA; 10195 MW; A34FDE21E6FA9C2E CRC64;

Query Match
Best Local Similarity 31.3%; Score 177.5; DB 11; Length 92;
Matches 35; Conservative 19; Mismatches 36; Indels 1; Gaps 1;

OY 11 MKVSAALLCLLMATFSPQGLAOPDSVSIPTCCFNVINKRIPQRLSYTRITNIQCP 70
DB 1 MKLCLSTLALLLLAEFCAPVTSAPRGSDPIISCFYSASRKLPNFTDYETSSL-CS 59
OY 71 KEAVIFKTRKGEVCADPKERWRDMSKHL 101
DB 60 KPAVVFLTRKRGVCAADPSPVWNEVYNDLE 90
```

```
RESULT 15
ID 095690 PRELIMINARY: PRT; 62 AA.
AC 095690;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CC-chemokine (Fragment).
GN CC-Chemokine.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bartels J.H., Schlueter C., Richter E., Noso N., Christophers E.,
RA Schroeder J.M.;
RT "Cloning of a novel human cDNA differing from typical CC-chemokines in
RT the deletion of 21 nucleotides encoding the third cysteine.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z77651; CAB01112.1;
DR HSSP: P80096; IBOO.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR SMART: SM00199; SCY; 1.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 62 AA; 7151 MW; 5F7D20AF359F4D2A CRC64;

Query Match
Best Local Similarity 30.5%; Score 173; DB 4; Length 62;
Matches 33; Conservative 12; Mismatches 16; Indels 8; Gaps 1;
```


GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 18, 2003, 03:07:17 : Search time 2869 Seconds

(without alignments)
8683.165 Million cell updates/sec

Title: US-10-033-067-2

Sequence: 1 aaacttcacccctcatgct.....actaaaaaaaaaaaaa 856

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlg_mus:*
34: em_hlg_pln:*
35: em_hlg_rod:*
36: em_hlg_mam:*
37: em_hlg_vrt:*
38: em_sy:*
39: em_hlgo_hum:*
40: em_hlgo_mus:*
41: em_hlgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	844.2	98.6	1368	9	HSY16645
2	841	98.2	878	9	HSMCPR02
3	589.6	68.9	181022	9	AC011193
4	586.4	68.5	2991	9	HSMCPR2
5	394.8	46.1	828	4	AF506972
6	393.2	45.9	839	4	S67954
7	359.6	42.0	833	4	SSPWCPR2
8	282.8	33.0	479	4	AF399641
9	257.6	30.1	1085	9	HSMCPR3A
10	256	29.9	810	6	HSMCP3
11	256	29.9	814	6	A17783
12	256	29.9	814	6	AR094458
13	244.6	28.6	767	4	EC4251189
14	238.8	27.9	813	9	HSCCHK53
15	237	27.7	839	9	HSU46573
16	235.6	27.5	807	9	HUMBOTAXIN
17	222	25.9	3338	4	S67956
18	221.4	25.9	725	9	HSMCP1
19	221.4	25.9	739	9	S71513
20	221.4	25.9	741	6	E05611
21	221.4	25.9	743	9	BC009716
22	220.2	25.7	514	4	BCA251188
23	219.8	25.7	741	6	A17786
24	219.8	25.7	741	6	AR094465
25	219.8	25.7	741	9	HUMMCAF
26	218.2	25.5	630	4	CFU29653
27	218	25.5	441	9	BC017850
28	216	25.2	771	4	BOVMOCHEM
29	214.8	25.1	661	9	S69738
30	214	25.0	740	4	SSPWCPR1
31	214	25.0	757	4	SSMCP1
32	210.6	24.6	718	9	HUMSECPA
33	205.4	24.0	399	6	BD003075
34	203	23.7	825	9	HSU46767
35	203	23.7	829	9	BC008621
36	203	23.7	855	9	HSSCYA13
37	203	23.7	860	9	HSU59808
38	201.2	23.5	317	4	BCA251190
39	200.8	23.5	300	9	AF255343
40	200.4	23.4	709	9	HSMCP4
41	199.2	23.3	300	9	AF276081
42	194.2	22.7	330	6	E02542
43	194.2	22.7	330	6	E03044
44	188.4	22.0	294	9	HSU34780
45	187.4	21.9	516	10	BC027520

ALIGNMENTS

RESULT 1
LOCUS HSY16645
DEFINITION Homo sapiens mRNA for monocyte chemotactic protein-2.
ACCESSION Y16645
VERSION Y16645.1 GI:2916795
KEYWORDS MCP-2 gene; monocyte chemotactic protein 2.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 1368)
Van Coillie,E., Proost,P., Van Aelst,I., Struyf,S., Polfliet,M., De Meester,I., Harvey,D.J., Van Damme,J. and Opdenakker,G.
Functional comparison of two human monocyte chemotactic protein-2

Pred. No. is the number of results predicted by chance to have a

isoforms, role of the amino-terminal pyroglutamic acid and processing by CD26/dipeptidyl peptidase IV
Biochemistry 37 (36), 12672-12680 (1998)
JOURNAL MEDLINE 98400973
PUBMED 9730840
REFERENCE 2 (bases 1 to 1368)
AUTHORS Van Collie,E.
TITLE Direct Submission
JOURNAL Submitted (23-FEB-1998) E. Van Collie, Rega Institute for Medical Research, Minderbroederstraat 10, 3000 Leuven, BELGIUM
COMMENT Related sequences: X99886, Y10802.
FEATURES
source
1..1368
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"
/map="q11.2"
/clone="HL142q"
/tissue_type="testis"
/clone_idb="Clontech"
473..772
/gene="MCP-2"
473..772
/gene="MCP-2"
/codon_start=1
/product="monocyte chemotactic protein-2"
/protein_id="CAA76341.1"
/db_xref="GI:2916796"
/db_xref="SWISS-PROT:P80075"
/translation="MKVSALLCLILMAAFSPQGLADPPSVSIPITCFENVIRKIP
IORLESYTRITNIQCPRKENVIFPKRKREKVCADPKEMVDSMKHLIDQINLKP"
473..541
/gene="MCP-2"
542..769
/gene="MCP-2"
/product="unnamed"
677
/note="polymorphism, Lys -> Gln"
/replace="c"
variation
BASE COUNT 457 a 292 c 243 g 376 t
ORIGIN
Query Match 98.6%; Score 844.2; DB 9; Length 1368;
Best Local Similarity 98.8%; Pred. No. 2.9e-157;
Matches 846; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
OY 1 AACCTTCACCTTCATGCTGAAGTCAACCTTGCCTCCCAAGATGAAGTTTCTGCA 60
|||||
Db 428 AACCTTCACCTTCATGCTGAAGTCAACCTTGCCTCCCAAGATGAAGTTTCTGCA 487
OY 61 GCGCTTCTGTCGCTGCTCATGGCAGCACTTTCAGCCCTCAGGACTTCTCAGCCA 120
|||||
Db 488 GCGCTTCTGTCGCTGCTCATGGCAGCACTTTCAGCCCTCAGGACTTCTCAGCCA 547
OY 121 GATTCAGTTTCCATTCACATACCTGCTGCTTTAAGCGTGATCAATGAAGAAATTCCTATC 180
|||||
Db 548 GATTCAGTTTCCATTCACATACCTGCTGCTTTAAGCGTGATCAATGAAGAAATTCCTATC 607
OY 181 CAGAGGCTGAGAGCTACACAGAATCACCAACATCCATGTCCTCAAGAGAGCTGTGATC 240
|||||
Db 608 CAGAGGCTGAGAGCTACACAGAATCACCAACATCCATGTCCTCAAGAGAGCTGTGATC 667
OY 241 TTCAAGACCAACAGGGGAGAGAGTGTGCTGACCCCAAGAGAGATGGGTCAGGGAT 300
|||||
Db 668 TTCAAGACCAACAGGGGAGAGAGTGTGCTGACCCCAAGAGAGATGGGTCAGGGAT 727
OY 301 TTCAATGAAGCATCTGGACCAATATTTCAAAATCTGAAGCCATGAGCCTTCTATATGGA 360
|||||
Db 728 TTCAATGAAGCATCTGGACCAATATTTCAAAATCTGAAGCCATGAGCCTTCTATATGGA 787
OY 361 CTGAGAGTCAGAGGCTTGAAGAAAGCTATTATTTCCCAAGCTCCCGGAGTGCAGT 420
|||||

Db 788 CTGACAGTCACAGCTTGAAGAAAGCTTATTTTCCCAAGCTCCCGGAGTGCAGT 847
OY 421 GTGACATTTATTTTATTAATACATCCACAAGAGATTTATTTAAATTAAGACATAA 480
|||||
Db 848 GTGACATTTATTTTATTAATACATCCACAAGAGATTTATTTAAATTAAGACATAA 907
OY 481 TATTTCTTAAAAAGATTTTATTTATTTTAACTGTGATGTTTAACTCTATCTGTCA 540
|||||
Db 908 TATTTCTTAAAAAGATTTTATTTATTTTAACTGTGATGTTTAACTCTATCTGTCA 967
OY 541 ACATCTGTGTAATTAATAAATCCCGTATGTTTGTGTTTGTTCCT 600
|||||
Db 968 ACATCTGTGTAATTAATAAATCCCGTATGTTTGTGTTTGTTCCT 1027
OY 601 GTGACCTCACTAAGTTTCACGGCCAAANGTCATGTTTCCCTCCACNGTMCAGTAG 660
|||||
Db 1028 GTGACCTCACTAAGTTTCACGGCCAAANGTCATGTTTCCCTCCACNGTMCAGTAG 1087
OY 661 TTGTGGGGTCCCTCCNGTATCATCAAGGTGAAGACATTAGTATTTTGGCAATCAGT 720
|||||
Db 1088 TTGTGGGGTCCCTCCNGTATCATCAAGGTGAAGACATTAGTATTTTGGCAATCAGT 1147
OY 721 GCTCCTGTAAGTCAAAATGTGCTGTTGTAAGCTGTTGTTGAATTTGANGTACTATA 780
|||||
Db 1148 GCTCCTGTAAGTCAAAATGTGCTGTTGTAAGCTGTTGTTGAATTTGANGTACTATA 1207
OY 781 TTAATATGGAATTTGAAAAAATTTTCAAAAAAGAAAAATATATATTTAAACATA 840
|||||
Db 1208 TTAATATGGAATTTGAAAAAATTTTCAAAAAAGAAAAATATATATTTAAACATA 1267
OY 841 AAAAAAAAAAAAAA 856
|||||
Db 1268 AAAAAAAAAAAAAA 1283
RESULT 2
HSMCPRO2 878 bp mRNA linear PRI 02-APR-1997
LOCUS
DEFINITION H.sapiens mRNA for monocyte chemotactic protein 2.
ACCESSION Y10802
KEYWORDS MCP-2 gene; monocyte chemotactic protein 2.
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
Van Collie,E., Froyen,G., Nomiyama,H., Miura,R., Filen,P., Van
Aelst,I., Van Damme,J. and Opendakker,G.
Human monocyte chemotactic protein-2: cDNA cloning and regulated
expression of mRNA in mesenchymal cells
Biochem. Biophys. Res. Commun. 231 (3), 726-730 (1997)
JOURNAL MEDLINE 97224420
PUBMED 9070881
REFERENCE 2 (bases 1 to 878)
AUTHORS Van Collie,E.
TITLE Direct Submission
JOURNAL Submitted (23-JAN-1997) E. Van Collie, Rega Institute for Medical Research, Minderbroederstraat 10, 3000 Leuven, BELGIUM
FEATURES
source
1..878
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"
/map="q11.2"
/clone="HL5005b"
/tissue_type="bone marrow"
/clone_idb="Clontech"
57..356
/gene="MCP-2"
57..356
/gene="MCP-2"
/codon_start=1


```

Db 169495 GATTCATGAAGCATCTGGACCAATATTTTCAAAATCTGAACCATGACCTTCATACAT 169436
QY 358 GGACTGAGAGTCAGAGCTTGAGAAAAGCTTATTTTCCCAACCTCCCGCAGGTGC 417
Db 169435 GGACTGAGAGTCAGAGCTTGAGAAAAGCTTATTTTCCCAACCTCCCGCAGGTGC 169376
QY 418 AGTGTGACATTTATTTATATACATCCACAAGAGATTTTAAATATTTAAAGCA 477
Db 169375 AGTGTGACATTTATTTATATACATCCACAAGAGATTTTAAATATTTAAAGCA 169316
QY 478 TAATATTTCTAAAAGATTTAATTAATTAAGTGTGATGTTTAACTATCTATCGT 537
Db 169315 TAATATTTCTAAAAGATTTAATTAATTAAGTGTGATGTTTAACTATCTATCGT 169256
QY 538 CATACATCTAGTGAATGTAATAATGCAAAATCTGATGATGTTTGTGTTTGTGTTT 597
Db 169255 CATACATCTAGTGAATGTAATAATGCAAAATCTGATGATGTTTGTGTTTGTGTTT 169196
QY 598 CTTGTGAGCTCACTAAGTTCAGGCCAANGTCAATTTCTCCCTCCACCGTNCATG 657
Db 169195 CTTGTGAGCTCACTAAGTTCAGGCCAANGTCAATTTCTCCCTCCACCGTNCATG 169136
QY 658 GTGTGTGGGGTCTCCCTCCGATCATCAAGTGAACACCTAGTATCTTTGGCAATC 717
Db 169135 GTGTGTGGGGTCTCCCTCCGATCATCAAGTGAACACCTAGTATCTTTGGCAATC 169076
QY 718 AGTGTCTCTGTAAGTCAAAATGTGCTTTGTACTGCTGTTTGAAATTTGANGTACTGT 777
Db 169075 AGTGTCTCTGTAAGTCAAAATGTGCTTTGTACTGCTGTTTGAAATTTGANGTACTGT 169016
QY 778 ANATACTATGGAATTTTGAATAAATTTCAAAAAAANATATATATATTTAAATA 837
Db 169015 ATATACTATGGAATTTTGAATAAATTTCAAAAAAANATATATATATTTAAATA 168956
QY 838 CTA 840
Db 168955 CTA 168953

RESULT 4
HSMCP2
LOCUS HSMCP2 2991 bp DNA linear PRI 20-MAR-1997
DEFINITION H.sapiens MCP-2 gene.
ACCESSION X99886
VERSION X99886.1 GI:1905800
KEYWORDS MCP-2 gene; monocyte chemotactic protein 2; SCYA10 gene.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Van Collie,E., Fiten,P., Nomiyama,H., Sakaki,Y., Miura,R.,
Yoshie,O., Van Damme,U. and Odenakker,G.
TITLE The human MCP-2 gene (SCYA8): cloning, sequence analysis, tissue
expression, and assignment to the CC chemokine gene contig on
chromosome 17q11.2
JOURNAL Genomics 40 (2), 323-331 (1997)
MEDLINE 97237052
PUBMED 9119400
REFERENCE
PUBMED 2 (bases 1 to 2991)
AUTHORS Odenakker,G.M.M.
TITLE Direct Submission
JOURNAL Submitted (07-AUG-1996) G.M.M. Odenakker, Rega Institute for
Medical Research, Minderbroedersstraat 10, B 3000 Leuven, BELGIUM
FEATURES
source
1..2991
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"
/map="q11.2"
209..219
/note="DR-A"
/rl_type=DIRECT
repeat_region

```

```

repeat_region 240..248
/note="DR-B"
/rl_type=DIRECT
CAAT_signal
296..300
repeat_region 310..318
/note="IR-A"
/rl_type=INVERTED
406..415
/note="DR-B"
/rl_type=DIRECT
407..416
/note="IR-B"
/rl_type=INVERTED
425..435
/note="DR-A"
/rl_type=DIRECT
429..437
/note="IR-B"
/rl_type=INVERTED
455..465
/note="IR-C"
/rl_type=INVERTED
467..472
/rl_type=INVERTED
492..502
/note="IR-C"
/rl_type=INVERTED
492..500
/note="IR-A"
/rl_type=INVERTED
join(534..639,1331..1448,1864..1969)
/gene="MCP-2 (SCYA10)"
join(534..639,1331..1448,1864..1969)
/gene="MCP-2 (SCYA10)"
/codon_start=1
/product="monocyte chemotactic protein-2"
/protein_id="CA068168.1"
/db_xref="GI:1905801"
/db_xref="SWISS-PROT:P80075"
/translation="MLKTLPLPSKKVSAALCLIMATFSPOGLAOPDSVIPITC
GFNVNIRKPIQRLSELYRITNIQCPKEAVIKTKGRKEVCADPERWVRDMSKHLDD
IFQNLKP"
534..639
/gene="MCP-2 (SCYA10)"
/number=1
640..1330
/gene="MCP-2 (SCYA10)"
/number=1
1331..1448
/gene="MCP-2 (SCYA10)"
/number=2
1449..1863
/gene="MCP-2 (SCYA10)"
/number=2
1864..1969
/gene="MCP-2 (SCYA10)"
/number=3
BASE COUNT 799 a 709 c 632 g 851 t
ORIGIN
Query Match 68.5%; Score 586.4; DB 9; Length 2991;
Best Local Similarity 97.8%; Pred. No. 36-106;
Matches 590; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 238 ATCTTCAGACCAACCAAGGGGCAAGAGTCTGTGCTGACCCCAAGAGAGATGGTCAG 237
Db 1862 ACCTTCAGACCAACCAAGGGGCAAGAGTCTGTGCTGACCCCAAGAGAGATGGTCAG 1921
QY 298 GATTCATGAAGCATCTGGACCAATATTTTCAAAATCTGAACCATGACCTTCATACAT 357
Db 1922 GATTCATGAAGCATCTGGACCAATATTTTCAAAATCTGAACCATGACCTTCATACAT 1981
QY 358 GGACTGAGAGTCAGAGCTTGAGAAAAGCTTATTTTCCCAACCTCCCGCAGGTGC 417

```

```

Db 1982 GCAGCTGACGCTAGACGCTTGAAGAAAAAGCTTATTTTCCCAACCTCCCGAGGTC 2041
QY 418 AGTGCACATATTTTATATTAACATCCAAAGAGATTATTTTAAATTAAGCA 477
Db 2042 AGTGCACATATTTTATATTAACATCCAAAGAGATTATTTTAAATTAAGCA 2101
QY 478 TAAATTTCTTAAAAAGTATTTTAAATTAATTAAGTGTGATTTTAACTATCTGT 537
Db 2102 TAAATTTCTTAAAAAGTATTTTAAATTAATTAAGTGTGATTTTAACTATCTGT 2161
QY 538 CATACATCTTACTGATGATGAAATGCAAAATCTGTGATGTGTTTGTGTTT 597
Db 2162 CATACATCTTACTGATGATGAAATGCAAAATCTGTGATGTGTTTGTGTTT 2221
QY 598 CCGTGAGCTCACTAGTACGACGCAAGANGCATGTTCTCCCTACCGTNGTGA 657
Db 2222 CCGTGAGCTCACTAGTACGACGCAAGANGCATGTTCTCCCTACCGTNGTGA 2281
QY 658 GTGTGTGGGGTCTCCCTGATCATCAAGTGAACAACCTTAGTATTTTGGCAATC 717
Db 2282 GTGTGTGGGGTCTCCCTGATCATCAAGTGAACAACCTTAGTATTTTGGCAATC 2341
QY 718 ACTGCTCTCTGATGATCAAAATGTGTCTTGTACTGCTGTGTTGAAATGANGTACTGT 777
Db 2342 ACTGCTCTCTGATGATCAAAATGTGTCTTGTACTGCTGTGTTGAAATGANGTACTGT 2401
QY 778 AATATACATGATGATTTTAAAAAAATTTCAAAAAAGAAATATATATTTAAAA 837
Db 2402 AATATACATGATGATTTTAAAAAAATTTCAAAAAAGAAATATATATTTAAAA 2461
QY 838 CTA 840
Db 2462 CTA 2464

RESULT 5
AF506972 828 bp mRNA linear MAM 22-MAY-2002
LOCUS AF506972
DEFINITION Equus caballus mcp-2 mRNA, complete cds.
ACCESSION AF506972.1 GI:21070220
VERSION
KEYWORDS
ORGANISM Equus caballus.
SOURCE Equus caballus.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
REFERENCE 1 (bases 1 to 828)
AUTHORS Takafuji,V.A., Sharova,L.V., Crisman,M.V. and Howard,R.D.
TITLE Equus caballus monocyte chemoattractant protein-2 (mcp-2), complete
cgs
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 828)
AUTHORS Takafuji,V.A., Sharova,L.V., Crisman,M.V. and Howard,R.D.
TITLE Direct Submission
JOURNAL Submitted (29-APR-2002) Large Animal Clinical Sciences, Orthopedic
Research Laboratory, VA-MD Regional College of Veterinary Medicine,
Virginia Polytechnic Institute and State University, Duckpond
Drive, Blacksburg, VA 24061, USA
FEATURES
SOURCE
1..828
/organism="Equus caballus"
/db_xref="taxon:9796"
/cell_type="LPS-stimulated peripheral blood mononuclear
cells"
46..345
/codon_start=1
/product="mcp-2"
/protein_id="AAM34214.1"
/db_xref="gi:21070221"
/translation="MKVSAALCLILTGVAFTHVAQDAVSIPVTCFQVDDKKVP
IQRVSYRIRSSQSEAVIFKTVYDKICADPKQKWDIMKRLDQSRPKP"
CDS
BASE COUNT 244 a 191 c 172 g 221 t
ORIGIN

```

```

Query Match 46.1%; Score 394.8; DB 4; Length 828;
Best Local Similarity 74.3%; Pred. No. 2,8e-68;
Matches 641; Conservative 0; Mismatches 179; Indels 43; Gaps 10;

QY 1 AATCCTTACCTCTCATGCTGAAAGCTCACACCTTGGCTCCAGATGAGGTTTGCA 60
Db 1 AATCCTTACCTCTCATGCTGAAAGCTCACACCTTGGCTCCAGATGAGGTTTGCA 60
QY 61 GCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Db 61 GCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
QY 121 GATTCAGTTTCCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 180
Db 121 GATTCAGTTTCCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 180
QY 181 CAGAGGCTGAGAGCTACACAGAGATCACACATTCATTCATTCATTCATTCATTCAT 240
Db 181 CAGAGGCTGAGAGCTACACAGAGATCACACATTCATTCATTCATTCATTCATTCAT 240
QY 241 TTCAAGACCAAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 300
Db 241 TTCAAGACCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 300
QY 301 TCCATGAGCATCTGAGCAAAATTTTCAAAATCTGAAGCCATGAGCCTTCATCATGGA 360
Db 301 TCCATGAGCATCTGAGCAAAATTTTCAAAATCTGAAGCCATGAGCCTTCATCATGGA 360
QY 361 CTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 415
Db 361 CTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 415
QY 416 GCAGTGTGATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 475
Db 416 GCAGTGTGATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 475
QY 476 CATATATTTCTTAAAGATTTTAAATTTATTTATTTATTTATTTATTTATTTATTTAT 534
Db 476 CATATATTTCTTAAAGATTTTAAATTTATTTATTTATTTATTTATTTATTTATTTAT 534
QY 534 TTTTCTGAGAGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 594
Db 534 TTTTCTGAGAGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 594
QY 595 TTTCTGAGAGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 653
Db 595 TTTCTGAGAGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 653
QY 654 CAGAGTGTGAGAGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 713
Db 654 CAGAGTGTGAGAGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 713
QY 714 AATCAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 773
Db 714 AATCAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 773
QY 774 CTTGATTAATCTATGATGATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 833
Db 774 CTTGATTAATCTATGATGATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 833
QY 834 AATCAGTAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 896
Db 834 AATCAGTAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 896
QY 896 TAAACTAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 954
Db 896 TAAACTAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 954

RESULT 6
S67954 839 bp mRNA linear MAM 23-SEP-1994
LOCUS S67954
DEFINITION monocyte chemoattractant protein-2 [clone c11/1] (cattle, blood
PMN's, mRNA, 839 nt).
ACCESSION S67954
VERSION S67954.1 GI:544998

```


OY	138	AATCAGCTCGTGGCTTTAAGTGATCAATAAGGAAATTCCTATTCCAGAGGCTGGACGTGA	197
Db	151		210
OY	198	CACAAGAATCACCAACATCATCAATGTGCCAAGGAAAGCTGTGATCTTCAAGACCAAACGGGG	257
Db	211		270
OY	258	CAGAAGGCTCTGTGCTGACCCCCAGAGAGATGGTCAAGGATTCATGAAACATCTGGA	317
Db	271		330
OY	318	CCAATATTTTAAAAATCGAAGCCATGAGCCCTCATACATGACACTGAGAG----TCAGAG	373
Db	331		390
OY	374	CTTGAAGAAAAGCTTATTTATTT---TTCCCAACCTCCCAGAGTGCAGTGTGACATTAT	430
Db	391		450
OY	431	TTTTATTATTAACATCCACAAGAAGATTTATTTTAAATTAATTAAGCATPATATTTCTTAA	490
Db	451		506
OY	491	AAAGTATTTATTTATTTATTTAGTTGTGATGTTTAACTGTTTAACTGCTGCTGA--TGCATCCTAG	549
Db	507		566
OY	550	TGAATGTAAATATGCAAAATCCCTGGTGTGATGTTTGTTTTGTTTTCTTCCGTGAGCTCA	609
Db	567		626
OY	610	ACTAAGTTCAGGGCCAAANGTCATTGTTCTCCCTCTTACCNSTNGTGTAGTGTGGGGT	669
Db	627		685
OY	670	CTCTCCNFGATCATCAACAGGTGAACACACTTAGGTATTCCTTGGCAATGCTCTCCTGTGA	729
Db	686		745
OY	730	AGTCAATATGTGTGCTTGTACTGCTGTTGTGAAATYGANGTGTACTGTANATTAACATATGG	789
Db	746	AGCCGAA-GTGGTGGGCAAGTATATTGTGTAAGTGTATGTTCACACACACTGTGGAGC	804
OY	790	AATTTTGAIAAAAAAATTTCAA AAA 813	
Db	805		
RESULT 8			
LOCUS	AF399641	479 bp	mRNA linear NAM 23-AUG-2001
DEFINITION	Bos taurus chemoattractant protein 2 mRNA, partial cds.		
ACCESSION	AF399641		
VERSION	AF399641.1 GI:15281828		
KEYWORDS			
SOURCE			
ORGANISM	Bos taurus.		
	Bos taurus		
	Eumariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;		
	Bovidae; Bovinae; Bos.		
	1 (bases 1 to 479)		
REFERENCE			
AUTHORS	Werling,D.		
JOURNAL	Role of chemokines in respiratory syncytial virus infection		
REFERENCE	Unpublished		
AUTHORS	2 (bases 1 to 479)		
TITLE	Werling,D.		
JOURNAL	Direct Submission		
FEATURES	Submitted (11-JUL-2001) Institute of Animal Sciences, ETH Zurich,		
	Schorenstrasse 16, Scherzenbach, ZH 8603, Switzerland		
source	Location/Qualifiers		
	I..479		

			/organism="Bos taurus"	
			/db_xref="taxon:9913"	
CDS		<1..303	/note="MCP-2; chemokine"	
			/codon_start=1	
			/product="chemoattractant protein 2"	
			/protein_id="AK94451.1"	
			/db_xref="GI:15281829"	
			/translation="MKRVSAIGLLVLAETGQVLADPDSVPITPCRSVINGRI PFKKLDYTRTNSQCPOEAFVFPTKDRDVCADPKOKWQTSIRLIDOKSRPKP"	
BASE COUNT	129 a	115 c	96 g	139 t
ORIGIN				
Query Match	33.0%	Score 282.8;	DB 4;	Length 479;
Best Local Similarity	77.1%;	Pred. No. 4.3e-46;		
Matches 373;	Conservative	0;	Mismatches 102;	Indels 9; Gaps 2;
Oy	43	AAGATGAAGGTTCCTGCACGGCGTTCTGTGCCCTGCCTCATAGGCGCACCACATTGACCCCT	102	
Dd	1	ACGATGAAGGTTCCTGCACGGCGTTCTGTGCCCTGCCTCATAGGCGCACCACATTGACCCAC	60	
Oy	103	CAGGACTGTGCTGCACGACGATTCAGTTCCATTCCAATCACCTGCTGCTTAACGTGATC	162	
Dd	61	CAGTGCTGCTGCACGACGATTCAGTTCTTCCACCAATCACCTGCTGCTTAAGTGTATC	120	
Oy	163	AATAGAATAATTCCTATCCAGAGGCTGAGAGCTACACAGATGACCAACATCCAAATGT	222	
Dd	121	AATGGAGAGATCCCTTCAGAGAGCTGGAGAGCTACAGAGATCACCACAGCCAGTGT	180	
Oy	223	CCCAGGAAGCTGTATCTTCAAGACCCAACGGGCGAAGGAGCTGTGCTGACCCCAAG	282	
Dd	181	CCCCGGAAGCTGTATCTTCAAGACCCAAGGGGAGGAGTGTGCTGACCCCAAG	240	
Oy	283	GAGAGATGGTTCAGGAGATTCATGAGAGATCTGCACCAATATTTCAAATTCGAGGCA	342	
Dd	241	CAGAGTGGTTCAGAGATTCATTCATAGGCTCTCGAGACCAAAATGCCGAACCGAAGCT	300	
Oy	343	TGAGCCTTCATCATGATGACGTGAGAGCTGAGAGCTTGAAGAAAAGCTTATTTATTTCCCA	402	
Dd	301	TGAACTTCATCATGATGACGTGAGAGAGAGCTTGAAGAAAATCTTATTTATTTCCCA	360	
Oy	403	ACCTCCCCCAGGTGCAGTGTGACATTTATTTATTTAACATCCACAAGAG-ATATTTGT	461	
Dd	361	ACCTTCCCCAGGT-----TATTTATTTATTTATTTATTTATTTATTTATTTATTT	412	
Oy	462	TAAATATTTAAGCATATATTTCTTTAAAAAGTATTTAATATATTTAAGTTGTGATG	521	
Dd	413	TTAAATATTTAAGCATATATTTCTTTAAAAAGTATTTAATATATTTAAGTTATTTGTTA	472	
Oy	522	TTTT 525		
Dd	473	TTTT 476		
RESULT 9				
LOCUS	HSMCP3A	1085 bp	mRNA	linear PRI 25-NOV-1998
DEFINITION	Homo sapiens mRNA for monocyte chemotactic protein-3 (MCP-3).			
ACCESSION	X72308 S57464			
VERSION	X72308.1 GI:3928270			
KEYWORDS	monocyte chemotactic protein 3.			
SOURCE	Homo sapiens.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 1085)			
REFERENCE	Opdenakker,G., Froyen,G., Piten,P., Proost,C.P. and Van Damme,J. Human monocyte chemotactic protein-3 (MCP-3): molecular cloning of the cDNA and comparison with other chemokines JOURNAL Biochem. Res. Commun. 191 (2), 535-542 (1993) MEDLINE 8461011 PUBMED 2 (bases 1 to 1085)			

AUTHORS Odenakker, G.M.
 TITLE Direct Submission
 JOURNAL Submitted (27-MAY-1993) G.M. Odenakker, Rega Institute, University of Leuven, Minderbroedersstraat 10, B-3000 Leuven, BELGIUM
 REFERENCE Odenakker, G., Fiten, P., Nys, G., Froyen, G., Van Roy, N., Speleman, F., Laereys, G., and Van Damme, J.
 TITLE The human MCP-3 gene (SCYA7): cloning, sequence analysis, and assignment to the C-C chemokine gene cluster on chromosome 17q11.2-q12
 JOURNAL Genomics 21 (2), 403-408 (1994)
 MEDLINE 94375065
 PUBMED 7916328
 COMMENT On Nov 26, 1998 this sequence version replaced gi:313707.
 FEATURES
 source location/Qualifiers
 1..1085
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 gene 299..810
 /gene="MCP-3"
 CDS 299..628
 /gene="MCP-3"
 /codon_start=1
 /product="monocyte chemotactic protein-3"
 /protein_id="CAA51055.1"
 /db_xref="GI:313708"
 /db_xref="SWISS-PROT:P80098"
 /translation="MKKMPSPSKMKASALLCLLTAAPSPGLOAPVGINSTTC CYRINKIKIKORLESYRRTTSSHCPRNAVIFRKLDKEICADPTQKWDPMKHLCK KTOPPKL"
 sig_peptide 299..397
 /gene="MCP-3"
 mat_peptide 398..625
 /gene="MCP-3"
 /product="monocyte chemotactic protein-3"
 polyA_signal 806..810
 /gene="MCP-3"
 BASE COUNT 314 a 214 c 229 g 328 t
 ORIGIN
 Query Match 30.1%; Score 257.6; DB 9; Length 1085;
 Best Local Similarity 67.9%; Pred. No. 4e-41;
 Matches 409; Conservative 0; Mismatches 179; Indels 14; Gaps 3:

Db 704 GGTCTGACATTAATTTTAACTTAATCTAAGCAATATGACCTTAATGATAATGCAAT 763
 Qy 476 CATAATATTTCTTAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 535
 Db 764 CATGGTTTCTTAGAGATTTAA-----AGTTATTAATTAATTAATTAATTAATCT 814
 Qy 536 GTCATACATCCATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 595
 Db 815 TCCATGATTTGGTGGTTTGAACATTAAGCTTGATGATGATGATGATGATGATGATGAT 874
 Qy 596 TT 597
 Db 875 GT 876
 RESULT 10
 HSMCP3 810 bp mRNA linear PRI 07-AUG-1993
 LOCUS HSMCP3
 DEFINITION H.sapiens NC28 mRNA for monocyte chemoattractant protein (MCP-3).
 ACCESSION X71087
 VERSION X71087.1 GI:288396
 KEYWORDS cytokine; monocyte-chemoattractant protein.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 810)
 Minly, A., Chalton, P., Guillemot, J.C., Kaghad, M., Liauzun, P., Magazin, M., Miloux, B., Minly, C., Ramond, P., Vite, N., Luper, J., Shire, D., Ferrara, P., and Caput, D.
 Molecular cloning of the MCP-3 chemokine gene and regulation of its expression
 Eur. Cytokine Netw. 4 (2), 99-110 (1993)
 JOURNAL 93305913
 MEDLINE 8318676
 PUBMED 2 (bases 1 to 810)
 REFERENCE Minly, A.
 AUTHORS Direct Submission
 TITLE Submitted (02-MAR-1993) A. Minly, Sanofi Elf Bio Recherches, Labège
 JOURNAL BP 137, 31676 Labège Cedex, FRANCE
 FEATURES
 source location/Qualifiers
 1..810
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /cell_type="peripheral blood monocytes"
 gene 41..370
 /gene="NC28"
 CDS 41..370
 /note="NC28"
 /note="alternative"
 /codon_start=1
 /product="monocyte chemoattractant protein (MCP-3)"
 /protein_id="CAA50405.1"
 /db_xref="GI:288397"
 /db_xref="SWISS-PROT:P80098"
 /translation="MKKMPSPSKMKASALLCLLTAAPSPGLOAPVGINSTTC CYRINKIKIKORLESYRRTTSSHCPRNAVIFRKLDKEICADPTQKWDPMKHLCK KTOPPKL"
 CDS 53..370
 /gene="NC28"
 /note="alternative"
 /codon_start=1
 /product="monocyte chemoattractant protein (MCP-3)"
 /protein_id="CAA50406.1"
 /db_xref="GI:288398"
 /db_xref="SWISS-PROT:P80098"
 /translation="MKKMPSPSKMKASALLCLLTAAPSPGLOAPVGINSTTC CYRINKIKORLESYRRTTSSHCPRNAVIFRKLDKEICADPTQKWDPMKHLCK KTOPPKL"
 CDS 71..370
 /gene="NC28"
 /codon_start=1

[illegible]

DEFINITION	Equus caballus mRNA for monocyte chemoattractant protein-1 (mcp-1 gene)					
ACCESSION	AJ251189					
VERSION	AJ251189.1 GI:6468532					
KEYWORDS	MCP-1 gene; monocyte chemoattractant protein-1.					
SOURCE	horse.					
ORGANISM	Equus caballus					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.					
AUTHORS	1 (bases 1 to 767) Benarafa,C., Cunningham,F.M., Hamblin,A.S., Horohov,D.W. and Collins,M.E.					
TITLE	Cloning of equine chemokines eotaxin, monocyte chemoattractant protein (MCP)-1, MCP-2 and MCP-4, mRNA expression in tissues and induction by IL-4 in dermal fibroblasts					
JOURNAL	Vet. Immunol. Immunopathol. 76 (3-4), 283-298 (2000)					
MEDLINE	21061912					
PUBMED	11044560					
REFERENCE	2 (bases 1 to 767)					
AUTHORS	Benarafa,C.					
TITLE	Direct Submission					
JOURNAL	Submitted (22-NOV-1999) Benarafa C., Department of Pathology and Infectious Diseases, The Royal Veterinary College, Hawkshead Lane, North Mymms, Hatfield, Hertfordshire AL9 7TA, United Kingdom					
FEATURES	Location/Oualifiers					
source	1..767 /organism="Equus caballus" /db_xref="taxon:9796" /tissue_type="Lung"					
gene	1..767 /gene="mcp-1"					
5'UTR	1..54 /gene="mcp-1"					
CDS	55..354 /gene="mcp-1" /codon_start=1 /product="monocyte chemoattractant protein-1" /protein_id="CAB61625.1" /db_xref="GI:6468533" /db_xref="SPTREMBL:O9TJ03" /translation="MKVSALLILCLLLAAAFSPQYLAOPALNSPYVCYTFNCKKRTIS SORAGSYKRVRTSSSKCREAVNIFFKIITLAKETICADPEQRWVDAYKQLDKKATPKP"					
sig_peptide	55..123 /gene="mcp-1"					
mat_peptide	124..351 /gene="mcp-1" /product="monocyte chemoattractant protein-1"					
3'UTR	355..767 /gene="mcp-1"					
BASE COUNT	232 a 176 c 149 g 210 t					
ORIGIN						
Query Match	28.6%; Score 244.6; DB: 4; Length 767;					
Best Local Similarity	65.5%; Pred. No. 1.5e-38;					
Matches 395; Conservative	0; Mismatches 194; Indels 14; Gaps 2;					
OY	1 AAACCTCACCTCTCATGCTGAAGCTGCACACCCTTGCCCTCAAGATGAAGTTTCGA 60					
Dd	10 A AACCAACAACATCTCAGGCCAAGCTCCCATCTTACCTCCAGCATGAAGTCTGTGCA 69					
OY	61 GCGETTCTGTGGCTGCTGCTCATGAGCGACGACCACTTTCAGCCCTCAGGACTTGTCAAGCCA 120					
Dd	70 GCCCTCCGTGCTGCTGCTCTCACCGCGGCCCTTCATCAGCACCAAGAGTCTGGTCAGGCCA 129					
OY	121 GATTCAGTTTCCATTCCAAATACCTGCTGCTTTAACGATGATCAATAGAAAATTCCTATYC 180					
Dd	130 GATCAATTAATTCTCCAGTCACCTGCTGCTATCATCTACCTACCGGTAGAAGATCTCAATCT 189					
OY	181 CAGAGGCGGAGAGTACACACAAGATAACCAACCAATTCATCCCAAGGAGAGCTGTGATTC 240					
Dd	190 CAGAGGCTGGGGAGACTATTAAGAAGTCAACGACGACGAAGTGTCCCAAAGAAGCTGTGTATC 249					
OY	241 TTCAAGACCAACGCGGGCAGAGAGGTCTGTCTGTGACCCCAAGGAGAGATGGTAGGAGAT 300					

```

|||||
250 TTCAGACCATATGGCCAGGAGATCTGTGTCGACCCGAGCAGAGAGTGGTCCAGAT 309
QY 301 TCCATACAGCATGTGGACCAATATTTCAAAATCTGAAGCCATGAGC-CTTCATACATGG 359
Db 310 GCGTGTAGACAGCTGGACCAAGAAAGCCCAAAAGCTTGAACACCTACTCCAAA 369
QY 360 ACTGAGAGTCAGAGCTTGAAGAAAGCTTATTTATTTCCCAACCTCCCGCCAGTGCAG 419
Db 370 GCCAGAGATGTAGAGCTAATTTATTTGCTCTGACATTCCTCCAAATGCCCTG----- 423
QY 420 TGTGACATATTTATTTAATACATCCCAAGAGATTTTAAATATTTAAGCATA 479
Db 424 -----ATTTATTTATTTATAGTTCAAGAGTATGAACTTTGTTATTTGACATGAAA 476
QY 480 ATTTTCTTAAAGATTTTATTTATTTAAGTTGTTGATGTTTAACTCATCTGTCA 539
Db 477 CTGTGAGCTTAAAGAGCTTAACTTTATTTAAGTTATGATTTAAAGTTATCTTCA 536
QY 540 TACATCTAGTGAATGAAATGCAAAATCCTGCTGATGTTTGTGTTTGTTC 599
Db 537 CGAATCTAGTGTCTGTGAGATATGAGACTTGAGCAAACTGCTTCTGTGAACCC 596
QY 600 TGT 602
Db 597 AGT 599

RESULT 14
HSCCHK53 813 bp mRNA linear PRI 10-SEP-1996
LOCUS HSCCHK53
DEFINITION H.sapiens mRNA for CC-chemokine, eotaxin variant (clone 53).
ACCESSION Z73568
VERSION 273568.1 GI:1531982
KEYWORDS CC-chemokine.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 813)
Bartels,J., Schluter,C., Richter,E., Noso,N., Kulke,R.,
Christophers,E. and Schroder,J.M.
Human dermal fibroblasts express eotaxin: molecular cloning, mRNA
expression, and identification of eotaxin sequence variants
Biochem. Biophys. Res. Commun. 225 (3), 1045-1051 (1996)
96374440
PUBMED 8780731
2 (bases 1 to 813)
Bartels,J.H.
Direct Submission
Submitted (04-JUL-1996) Bartels J. H.,
Christian-Albrechts-Universitaet zu Kiel, Dermatology/Hauklinik,
Mol. Biol. Lab. 609, Schittenhelmstr. 7, Kiel, Schleswig-Holstein,
Germany, D-24105

FEATURES
source
1..813
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="53"
/sex="Male"
/cell_type="fibroblast"
/tissue_type="foreskin"
<1..>813
/product="CC-chemokine"
/note="eotaxin-variant"
/evidence="experimental"
56..349
/note="eotaxin sequence variant"
/codon_start=1
/product="CC-chemokine"
/protein_id="CAA9997.1"
/db_xref="GI:1531983"
/db_xref="SWISS-PROT:P51671"

```

```

/translation="MKVSAALLMLLIAAFSPDGLGPASVPTCCFNLANRKIPLO
RLESYRIRTSKGKPEQKAVIRFKTLANIKADPKRWQDSMKYIDKQSPPKP"
sig_peptide
56..109
mat_peptide
110..346
/product="CC-chemokine"
/function="putative chemottractant protein"
/note="eotaxin variant"
3'UTR
347..>813
misc_RNA
508..517
/note="Two AUUA pentanucleotides arranged in tandem
within a U-rich region typical for short lived
mRNAs"
polyA_signal
734..739
/note="uncommon ATTA signal"
polyA_signal
766..771
/note="uncommon CATAA signal"
misc_RNA
782..786
/note="AUUA pentanucleotide, typical for short lived
cytokine mRNAs"
BASE COUNT 251 a 197 c 143 g 222 t
ORIGIN
Query Match 27.9%; Score 238.8; DB 9; Length 813;
Best Local Similarity 64.6%; Pred. No. 2.1e-37;
Matches 452; Conservative 0; Mismatches 231; Indels 17; Gaps 6;
QY 1 AACCTTCACCTTCATGCTGAAGCTCAGACCTTGGCCCTCAGATGAGTTCTGCA 60
Db 11 AAACCTCACCTTCACGCGCAAGACCTCAGCTTCACATCAATCAAGTCCGCA 70
QY 61 GCGGCTTCGCGCGCGCGCTGATGAGCGACCTTCAGCCCTCAGGACTGCTGCGCA 120
Db 71 GCACCTTCGTGGCTGCTGCTGCTATGACGCTGCTTACGCCGCCAGGGCTCAGGCCA 130
QY 121 GATTCACTTCCATTCACATCACCCTGCTTTAAGTGATCAATGAGAAATTCCTATC 180
Db 131 GCTTCTG-----TCCACACACCGTGGCTTTAAGCTGGCAATGAGAAATACCCCT 184
QY 181 CAGAGGCTGAGAGCTTACACAGAATACCAACATCATATGTTCCAGAGAGCTTGATC 240
Db 185 CAGGAGTAGAGAGCTCAGAGAGATCACAGTGAATATGTCCTCCCAAGAGCTGTATC 244
QY 241 TTCAAGACCAAGGGGGAAGAGAGTCTGTGACCCCAAGAGAGATGGGTGAGGAT 300
Db 245 TTCAAGACCAAGCGCCCAAGATATCTGTGCGGCCCAAGAGAGGTGGTAGAGAT 304
QY 301 TCCATGAAGCATCTGAGCAATATTTCAAAATCTGAAGCATGAGCCTTCATACA--TG 358
Db 305 TCCATGAAGTATCTGAGCAAAATCTCCAACTCCAAACATTAATATACATTTT 364
QY 359 GACTGAGAGTCAGAGCTTGAAGAAAGCTTATTTTCCCAACCTCCCGCAGTGCA 418
Db 365 GAACCAACACAGAGCGCTGAGTGTGCTTAATGTTTTC-----CTTCTTACAATCA 419
QY 419 GTGAGCATTTATTTATTAATACATCCACAAGA-GATTATTTTAAATTAATTAAGA 477
Db 420 TTCTGAGTAACTCATATTCATGTCACCAAGGCAAGGGGTTTATATATATATATA 479
QY 478 TAATATTTCTTAAAGATTTAATTAATTAATTAATTAATTAATTAATTAATTAAT 536
Db 480 TATTTTATTTTAAAGAAAGATTAATTAATTAATTAATTAATTAATTAATTAAT 539
QY 537 TCATACACTCTAGTGAATGATAAATGCAAAATCCTGGTATG--TGTTTTTGTGTTTGT 594
Db 540 CCATGAATATATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 599
QY 595 TTTCTGTGAGCTCAACTAATGATCAAGGCCCAAGATCATGTTGTCCTCCCTACG 654
Db 600 GCCCAATTCGATCCCTGTCAGCGTGTGGCAATGTTCCCTCTCTCTCTCTCT 659
QY 655 GTAGTGTGTGGGTGCGCCCGTGGATCATCAAGGTGAAA 694
Db 660 GGAATCTTTAAAGGTCTCTGCGCAAGATGATCATGATGAAA 699

```

```

Db      243  TTCAGACCAAACTGGCCCAAGGATATCTGTGGCCAGCCCAAGAAGAGTGGGTCAAGAT 302
Oy      301  TCCATGAAGCATCTGTGACCAAAATATTTCCAAAATCTGAAGCCATGACCTTCATCATG-- 358
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      303  TCCATGAAGTATCTGTGACCAAAAATCTCCAACTCCAAAGCCATTAATTAATCACCATTTTT 362
Oy      359  GACGACAGTCAGAGCTTGAAGAAAGCTTATTTATTTCCCAACCTCCGCCAGGTGCA 418
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      363  GAAACCAAAACGACGAGCCTGTGAGTGGCTTAATTTGTTTTTC---CCTCTTACAAATGCA 417
Oy      419  GTGTGACATTATTTTATTTATATCAATCCACAAGA-GATATATTTTAAATTAATTAAGCA 477
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      418  TTTCGAGAGTAACCTCATTTATTCAGTCCAAAGGCGATGGGTTTATATATATATATATATA 477
Oy      478  TAAATATTTCTTAAAAAGATTTTAAATATATTTAAGTTGTGATGTTTAACTC-TATCTG 538
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      478  TATTTTATTTTAAAAAAAAGCATTTGCATTTTATTTAATGAGCTTTAAAAACTTATTCCT 537
Oy      537  TCATATACCTCTAGTGAATGTAAATGCAAAATCCTGGTGATGTGTTTTT 585
      ||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      538  CCAATGAATATCATGTTATTTTAAACGTAAAGCTTTGTGACGATTCCTT 586

```

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 18, 2003, 03:06:02 ; Search time 262 Seconds

(without alignments)
7357.674 Million cell updates/sec

Title: US-10-033-067-2

Perfect score: 856
Sequence: 1 aaacctcactctcatgct.....actaaaaaaaaaaaaa 856

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2165239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_101002:*

1: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	849	99.2	856	19	AAV09218
2	841	98.2	2738	21	AAV74886
3	588.8	68.8	9475	24	ABK70707
4	378.4	44.2	411	18	AAV91023
5	257.6	30.1	1085	21	AAV21017
6	257.6	30.1	1085	21	AAV21018
7	257.6	30.1	1085	21	AAV74887
8	257.6	30.1	1085	21	AAA34895
9	257.6	30.1	1085	21	AAA34896

10	257.6	30.1	1085	24	ABK84649	Human cDNA differe
11	257.6	30.1	1706	22	AAK44714	Full-length polynu
12	257.6	30.1	5865	21	AAV21020	Human low adenosi
13	257.6	30.1	5865	21	AAV34898	Human adenosine re
14	256	29.9	810	21	AAV21016	Human low adenosi
15	256	29.9	810	21	AAA34894	Human adenosine re
16	256	29.9	814	21	AAV25259	Human adenosine re
17	254.4	29.7	810	16	AAV05371	Cytokine encoded b
18	250	29.2	250	21	AAA34840	Chemottractant pr
19	244	28.5	256	19	AAV09221	Human secreted exp
20	237	27.7	839	21	AAV74879	Human MC proprotel
21	235.6	27.5	807	21	AAV20924	Human chemokine co
22	235.6	27.5	807	21	AAV34802	Human ectaxin poly
23	235.6	27.5	859	18	AAV29944	Human adenosine re
24	235.6	27.5	3756	21	AAV20927	Human eosinocyte c
25	235.6	27.5	3756	21	AAA34805	Human ectaxin poly
26	235.6	27.5	209273	21	AAV21437	Human adenosine re
27	233.2	27.2	605	24	ABN6336	Human factor-relat
28	222.6	26.0	1712	19	AAV34249	Human ectaxin enco
29	222.6	26.0	1822	19	AAV34248	Human secreted pro
30	221.4	25.9	725	16	AAV05370	Human secreted pro
31	221.4	25.9	725	16	AAV05370	Chemottractant pr
32	221.4	25.9	802	20	AAV23515	Monocyte chemotatr
33	219.8	25.7	741	13	AAV30748	Human prostate can
34	219.8	25.7	741	21	AAV21021	PMCT7. Synthetic
35	219.8	25.7	741	21	AAA34899	Human low adenosi
36	218.8	25.6	738	10	AAV91337	Human adenosine re
37	218.2	25.5	739	19	AAV10341	DNA which encodes
38	218	25.5	787	13	AAV27946	Sequence encoding
39	216.2	25.3	2281	22	AAV2896	Human polynucleoti
40	214.8	25.1	661	21	AAV74882	Human chemokine co
41	213	24.9	236	19	AAV09219	Human MC proprotel
42	209.6	24.5	386	21	AAA3570	Human secreted exp
43	208.4	24.3	330	24	AAV38341	Coding sequence of
44	207.8	24.3	435	24	ABV57865	Human colon cancer
45	206.6	24.1	382	20	AAV68197	EST clone M100. H

ALIGNMENTS

RESULT 1	
AAV09218	
ID	AAV09218 standard; DNA: 856 BP.
XX	XX
AC	AAV09218;
XX	XX
DT	09-JUN-1998 (first entry)
XX	XX
DE	Human MC proprotein cDNA.
XX	XX
KW	Human monocytic chemotactic proprotein; MCP. Incyte clone; allergy;
KW	macrophage; diagnostic assay; body fluid; lung; biopsy;
KW	autoimmune disease; AIDS; asthma; rheumatoid arthritis; NIDDM;
KW	breast cancer; bladder; ss.
XX	XX
OS	Homo sapiens.
XX	XX
FH	Key
FT	Location/Qualifiers
FT	16..345
FT	/*tag" a
FT	/product= "monocyte chemotactic proprotein"
XX	XX
PN	W09802459-A1.
XX	XX
PD	22-JAN-1998.
XX	XX
PF	15-JUL-1997; 97WO-US12349.
XX	XX
PR	15-JUL-1996; 96US-0683655.
XX	XX
PA	(INCY-) INCYTE PHARM INC.
XX	XX

PI Au-Young J, Coleman R, Hillman JL;
 XX WPI: 1998-110529/10.
 DR P-PSDB; AAM42072.
 XX
 PT New human monocyte chemotactic protein - has homology to CC
 PT chemokine(s) useful for identifying agent for treating auto-immune
 PT diseases or allergic responses
 XX
 PS Claim 4; Page 39; 53pp; English.
 XX
 CC The human monocyte chemotactic protein cDNA sequence given was
 CC first identified in Incyte clone 965517 from a breast cDNA library.
 CC Antisense nucleotides can be used to control human MCPP expression
 CC especially where it may lead to inappropriate monocyte or macrophage
 CC activity causing damage associated with allergic responses to organs
 CC such as the lungs. Antisense nucleotides and MCPP cDNA may be used
 CC in diagnostic assays of body fluids or biopsied tissues to detect
 CC expression levels of MCPP. MCPP cDNA may also be useful for
 CC treatment of disorders such as asthma, rheumatoid arthritis, NIDDM
 CC or cancer of the breast or bladder. Human MCPP protein can be used to
 CC identify agonists, antagonists or inhibitors to modulate the activity of
 CC MCPP in allergic responses or autoimmune diseases such as AIDS.
 XX
 SO Sequence 856 BP; 261 A; 175 C; 157 G; 256 T; 7 other:
 Query Match 99.2%; Score 849; DB 19; Length 856;
 Best Local Similarity 100.0%; Pred. No. 3.4e-161;
 Matches 856; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AACCTTCACCTTCATGCTGAAGTCAACACCTTGGCCCTCAGAGTGAAGTTTGTGCA 60
 DB 1 AACCTTCACCTTCATGCTGAAGTCAACACCTTGGCCCTCAGAGTGAAGTTTGTGCA 60
 QY 61 GCGCTTCTGCTGCTGCTCTATGGAAGCACTTTCAGCCCTCAGGACTGTGCA 120
 DB 61 GCGCTTCTGCTGCTGCTCTATGGAAGCACTTTCAGCCCTCAGGACTGTGCA 120
 QY 121 GATTCAATTTTCATTCATCAATCACTGCTGCTTAAAGTATCAATAGAAAATTCCTATC 180
 DB 121 GATTCAATTTTCATTCATCAATCACTGCTGCTTAAAGTATCAATAGAAAATTCCTATC 180
 QY 121 GATTCAATTTTCATTCATCAATCACTGCTGCTTAAAGTATCAATAGAAAATTCCTATC 180
 DB 121 GATTCAATTTTCATTCATCAATCACTGCTGCTTAAAGTATCAATAGAAAATTCCTATC 180
 QY 181 CAGAGCTGAGAGCTGACACAGAAATCAACCAATCCATCCCAAGAGAGCTGTATC 240
 DB 181 CAGAGCTGAGAGCTGACACAGAAATCAACCAATCCATCCCAAGAGAGCTGTATC 240
 QY 241 TTCAGACCAAAACGAGGCAAGAGAGTGTGCTGACCCCAAGAGAGATGGTCAAGGAT 300
 DB 241 TTCAGACCAAAACGAGGCAAGAGAGTGTGCTGACCCCAAGAGAGATGGTCAAGGAT 300
 QY 301 TTCATGAAGCATCTGACCAAAATTTTCAAAATCTGAAGCATGAGCCTTATACATGA 360
 DB 301 TTCATGAAGCATCTGACCAAAATTTTCAAAATCTGAAGCATGAGCCTTATACATGA 360
 QY 361 CTGAGAGTCAAGAGCTTGAAGAAAAGCTTATTTTCCCAACCTCCCAAGGAGCAGT 420
 DB 361 CTGAGAGTCAAGAGCTTGAAGAAAAGCTTATTTTCCCAACCTCCCAAGGAGCAGT 420
 QY 421 GTGACATTTATTTTATTAATCATCCACAAGAGATTTATTTTAAATATTTAAAGCATAA 480
 DB 421 GTGACATTTATTTTATTAATCATCCACAAGAGATTTATTTTAAATATTTAAAGCATAA 480
 QY 481 TATTTCTTAAAGATATTTATTTATTTTAAAGTGTGATGTTTAACTATCTGTCAT 540
 DB 481 TATTTCTTAAAGATATTTATTTATTTTAAAGTGTGATGTTTAACTATCTGTCAT 540
 QY 541 ACATCTAGTGAATGTAAATGCAAAATCCGTGATGTTTGTGTTTGTGTTTCT 600
 DB 541 ACATCTAGTGAATGTAAATGCAAAATCCGTGATGTTTGTGTTTGTGTTTCT 600
 QY 601 GTGAGCTCAACTAAGTTCACGCGCAAAAGTATGTTCTCCCTCTACACNGTNGTACTG 660
 DB 601 GTGAGCTCAACTAAGTTCACGCGCAAAAGTATGTTCTCCCTCTACACNGTNGTACTG 660

QY 661 TTGAGGCTCCCTCCNTGATCATCAAGTGAACACTTAGGTATCTTGGCAATCACT 720
 DB 661 TTGAGGCTCCCTCCNTGATCATCAAGTGAACACTTAGGTATCTTGGCAATCACT 720
 QY 721 GCTCCTGTAACTCAAAATGTGCTGCTTGTACTGCTGTTGTGAATGTGACTGTANA 780
 DB 721 GCTCCTGTAACTCAAAATGTGCTGCTTGTACTGCTGTTGTGAATGTGACTGTANA 780
 QY 781 TAACTATGGAATTTTGAAGAAAAATTTCAAAAAGAAAAATATATATTTAAACTA 840
 DB 781 TAACTATGGAATTTTGAAGAAAAATTTCAAAAAGAAAAATATATATTTAAACTA 840
 QY 841 AAAAAAAAAAAAAA 856
 DB 841 AAAAAAAAAAAAAA 856
 RESULT 2
 ID AAA74886 standard; DNA; 2738 BP.
 AC AAA74886;
 XX
 DT 17-JAN-2001 (first entry)
 XX
 DE Human chemokine MCP-2 coding sequence SEQ ID NO: 80.
 XX
 KW Macrophage recruitment; chemokine derivative; MCP-1; osteoporosis;
 KW monocyte chemoattractant protein-1; inflammation; atherosclerosis; HIV;
 KW AIDS; stroke; psoriasis; autoimmune disease; hypertension; endotoxemia;
 KW basophil-mediated disease; myocardial infarction; acute ischaemia;
 KW rheumatoid arthritis; contraception; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 123..356
 FT /*tag= a
 FT /*product= "human chemokine"
 FT /*transl_except= (pos:261..263, aa:Gln)
 XX
 PN W0200042071-A2.
 XX
 PD 20-JUL-2000.
 XX
 PF 12-JAN-2000; 2000WO-US00821.
 XX
 PR 12-JAN-1999; 99US-0229071.
 PR 17-MAR-1999; 99US-0271192.
 PR 01-DEC-1999; 99US-0452406.
 XX
 PA (NEOR-) NEORX CORP.
 XX
 PI Grainger DJ, Tatalick LM;
 XX WPI: 2000-499101/44.
 DR P-PSDB; AAB15786.
 XX
 PT New peptide 3, amide and heterocyclic compounds and saccharide
 PT conjugates used for inhibiting chemokine induced activity and for
 PT treating e.g. stroke, vascular diseases, autoimmune diseases and tumour
 PT growth -
 XX
 PS Disclosure; Page 378-379; 387pp; English.
 XX
 CC The present invention concerns the identification of a number of
 CC chemokines which can be used to produce derivatives, agonists and
 CC antagonists which are then useful in disease treatment. The chemokines
 CC include sequences AAB15785-B15794, AAB15803-B15813 and AAB15831-B15848.
 CC These chemokine derivatives can be used to treat diseases such as
 CC autoimmune diseases, atherosclerosis, osteoporosis, HIV infection and
 CC AIDS, psoriasis, inflammatory diseases, hypertension, basophil-mediated

PD 21-MAR-2002.
XX 17-SEP-2001; 2001WO-US29332.
XX 15-SEP-2000; 2000US-232755P.
XX (GENA-) GENAISANCE PHARM INC.
PA Anastasio AE, Chew A, Han J, Lee HH;
PI WPI: 2002-371973/40.
DR P-PSDB; ABG35167.
XX
XX New genetic variants of Small Inducible Cytokine Subfamily A (Cys-Cys),
PT Member 8 (Monocyte Chemotactic protein) isogenes, useful for improving
PT efficiency and reliability in drug development for treating diseases -
PS
PS Claim 21; Fig 1; 84pp; English.
XX
XX The present invention relates to novel single nucleotide polymorphisms
CC (SNPs) in the human small inducible cytokine subfamily A (Cys-Cys),
CC member 8 (monocyte chemotactic protein) (SCYA8) gene located on
CC chromosome 17, and methods for haplotyping and/or genotyping the SCYA8
CC gene. The methods of the invention make use of allele-specific
CC oligonucleotides (ASOs) as probes and primers and/or primer-extension
CC oligonucleotides for detecting the SCYA8 gene polymorphisms. The
CC polynucleotides and screened compounds are useful for the treatment of
CC diseases associated with SCYA8 activity, such as inflammatory diseases
CC and human immunodeficiency virus (HIV) infection. The present sequence
CC represents a reference sequence for the human SCYA8 gene which shows
CC the variations in the gene.
XX
XX Sequence 9475 BP; 2863 A; 1898 C; 1777 G; 2925 T; 12 other:
S0
Query Match 68.8%; Score 588.8; DB 24; Length 9475;
Best Local Similarity 97.8%; Pred. No. 8.4e-109;
Matches 590; Conservative 2; Mismatches 11; Indels 0; Gaps 0;
OY 238 ATCTTCAGACCAAGCGGGGAGAGGCTGCTGCTGACCCCAAGAGAGAGTGGTCAGG 297
DB 5369 AGCTTCAGACCAAGCGGGGAGAGGCTGCTGCTGACCCCAAGAGAGATGGTCAGG 5428
OY 298 GATTCACGACGACATCGACCAATATTCGAAATCTCAAGCAGACCTTCATACAT 357
DB 5429 GATTCACGACGACATCGACCAATATTCGAAATCTCAAGCAGACCTTCATACAT 5488
OY 358 GACCTGAGAGTGAAG 417
DB 5489 GACCTGAGAGTGAAG 5548
OY 418 AGTTCGACATATTTATTAATCATCCAAAGAGATTTTAAATATTTAAAGCA 477
DB 5549 AGTTCGACATATTTATTAATCATCCAAAGAGATTTTAAATATTTAAAGCA 5608
OY 478 TAAATATTTTAAAGATTTTAAATATTTTAAATATTTTAAATATTTTAAATATTT 537
DB 5609 TAAATATTTTAAAGATTTTAAATATTTTAAATATTTTAAATATTTTAAATATTT 5668
OY 538 CATACATCTAGTGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 597
DB 5669 CATACATCTAGTGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 5728
OY 598 CCTGTGAGCTCAAGTCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCA 657
DB 5729 CCTGTGAGCTCAAGTCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGG 5788
OY 658 GTGTGTGGGGCTCCCTCCGATCATCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCA 717
DB 5789 GTGTGTGGGGCTCCCTCCGATCATCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCA 5848
OY 718 AGTTCGACATATTTATTAATCATCCAAAGAGATTTTAAATATTTTAAAGCA 777
DB 5849 AGTTCGACATATTTATTAATCATCCAAAGAGATTTTAAATATTTTAAAGCA 5908

OY 778 ANATACTATGCAATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 837
DB 5909 ATATTAATCTATGCAATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5968
OY 838 CTA 840
DB 5969 CTA 5971
RESULT 4
AAT91023
ID AAT91023 standard; cDNA; 411 BP.
XX
XX AAT91023;
AC
XX 16-FEB-1998 (first entry)
DT
XX
XX Human beta-chemokine H1305 (MCP-2) cDNA.
DE
XX
XX H1305; MCP-2; chemokine; human; chemottractant; chemotaxis;
KW virus infection; HIV; therapy; wound healing; ds.
XX
XX Homo sapiens.
OS
FH Key location/Qualifiers
FT CDS 47..376
FT /tag= a
PN
XX MO9725427-A1.
PD 17-JUL-1997.
XX
XX 10-JAN-1997; 97WO-US00379.
PF
XX 12-JAN-1996; 96US-0586395.
PR
XX (GENE) GENETICS INST INC.
PA
XX Lavalie ER, McCoy JM, Racle LA;
PI WPI: 1997-372866/34.
DR P-PSDB; AAW26655.
XX
XX New human beta-chemokine, H1305 and corresponding DNA - used in the
PT treatment of viral infection, e.g. HIV, and in wound healing
XX
XX Claim 1; Page 12-13; 21pp; English.
PS
XX This novel isolated polynucleotide, the coding sequence of which is
CC claimed, codes for human beta-chemokine H1305 (see AAW26655). A
CC partial clone for H1305 was isolated from a human peripheral blood
CC mononuclear cell (PBMC) cDNA library using methods that are
CC selective for secreted proteins. The partial clone was then used
CC to identify the full-length clone (deposited as ATCC 69968) from a
CC PBMC library. Also claimed are: (1) a host cell, preferably
CC mammalian, transformed with a H1305 polynucleotide operably linked
CC to an expression control sequence; (2) a recombinantly produced
CC H1305 protein; and (3) a composition comprising an antibody which
CC specifically reacts with the H1305 protein. The H1305 protein
CC (also known as MCP-2) may be used in a composition for the treatment
CC of a mammalian subject (claimed). It is thought to have chemokine
CC activities and may therefore have an effect on chemotaxis or
CC migration of blood cells. It may be useful for inhibiting viral
CC replication, including replication of HIV, and may also be used for
CC treatment of wounds and to raise monoclonal and polyclonal
CC antibodies which specifically react with H1305.
XX
XX Sequence 411 BP; 116 A; 112 C; 93 G; 90 T; 0 other;
S0
Query Match 44.2%; Score 378.4; DB 18; Length 411;
Best Local Similarity 99.7%; Pred. No. 7.3e-67;
Matches 379; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 536 GTCATACCTCTAGTGAATGTAAAAATGCAAAATCCTGTCGATGCTGTTTGTGTTTGT 595
 DB 815 TCCATGAGATTTTGGTGGGTTTGAACATTAACGCTTGATATGATCATCTCACTGCT 874
 OY 596 TT 597
 DB 875 GT 876
 RESULT 6
 AAF21018
 ID AAF21018 standard; DNA: 1085 BP.
 AC AAF21018;
 XX 14-MAR-2001 (first entry)
 DT
 XX Human low adenosine antisense oligonucleotide related sequence #2585.
 XX Low adenosine antisense oligonucleotide: phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiallergic; hypotensive; cyostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX Homo sapiens.
 OS
 XX MO200062736-A2.
 PN 26-OCT-2000.
 PD 24-MAR-2000; 2000MO-US08020.
 PE 06-APR-1999; 99US-0127958.
 PR (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 XX Nyce JW;
 PI WPI: 2000-679539/66.
 DR Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -
 PT
 PS Disclosure: Page 829-830; 1592pp; English.
 XX The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (1) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal or alternative base.
 CC (1) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiallergic, hypotensive and cyostatic activities.
 CC The antisense oligonucleotides and (1) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, such as stimulating factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)

CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention.
 XX
 SQ Sequence 1085 BP; 314 A; 214 C; 229 G; 328 T; 0 other;
 Query Match 30.1%; Score 257.6; DB 21; Length 1085;
 Best Local Similarity 67.9%; Pred. No. 1.5e-42;
 Matches 409; Conservative 0; Mismatches 179; Indels 14; Gaps 3;
 OY 1 AAACCTTCACTCTCATGCTGTAAGCTACAGCCCTTCCCTCAAGATGAAGTTTGTCA 60
 DB 284 AAACCTTCACTCTCATGCTGTAAGCTACAGCCCTTCCCTCAAGATGAAGCTTGTCA 343
 OY 61 GCGCTTCTGCTGCTGCTCATGCGACGACCTTTAGCCCTTAGGACTTGTCTACGCCA 120
 DB 344 GCACCTTCTGCTGCTGCTCATGCGACGCTGCTTTAGCCCTTAGGACTTGTCTACGCCA 403
 OY 121 GATTCAGTTTCATTCACATTCACCTGCTGCTTAAAGTATCATTAAGAAATTCCTATC 180
 DB 404 GTTGGATTAATTCCTCAACTACCTGCTGCTACAGATTAATTAAGAAATTCCTATC 463
 OY 181 CAGAGCTGAGAGCTACACAGAAATACACATCCATGATCCCAAGAGCTGTGATC 240
 DB 464 CAGAGCTGAGAGCTACAGAAAGGACACACAGTACGACACTGCCCGGAAGCTGTATC 523
 OY 241 TTCAGACCAAAAGGGGCAAGAGGCTGTGCTGACCCCAAGAGAGATGGCTCAGGAT 300
 DB 524 TTCAGACCAAAAGGGGCAAGAGGCTGTGCTGACCCCAAGAGAGTGGCTCAGGAC 583
 OY 301 TCCATGACATCTGACCAAAATTTCAAAATCTGAGAGCTGATGATCATACATGGA 360
 DB 584 TTTATGACATCTGACCAAAATTTCAAAATCTGAGAGCTGATGATCATACATGGA 643
 OY 361 CTGAG----AGTCAGACTTGAAGAAAGCTTATTTATTTCCCAACTCCCCAGAGTG 416
 DB 644 CTGAAACCAAGCATGACTTGAAGAAATATTTGTATACCTGCTTCTGCAGAGT 703
 OY 417 CAGTGTACATTTATTTATTAATCAATCCACAAGA-GATTATTTTAAATTAATTAAG 475
 DB 704 GGTTCAGATTTATTTATTAATCAATCCACAAGA-GATTATTTTAAATTAATTAAGT 763
 OY 476 CATATATTTCTTAAAAAGTATTTATTTAAGTTGTGATGTTTAAGCTATCT 535
 DB 764 CATGTTTCTTCTTAAATTTTAA-----AGTTATTAATTAATTTAAATTTAATCT 814
 OY 536 GTCATACCTCTAGTGAATGTAAAAATGCAAAATCCTGTCGATGCTGTTTGTGTTTGT 595
 DB 815 TCCATGAGATTTTGGTGGGTTTGAACATTAACGCTTGATATGATCATCTCACTGCT 874
 OY 596 TT 597
 DB 875 GT 876
 RESULT 7
 AAF74887
 ID AAF74887 standard; DNA: 1085 BP.
 AC AAF74887;
 XX 17-JAN-2001 (first entry)
 DT
 XX Human chemokine MCP-3 coding sequence SEQ ID NO: 81.
 DE Macrophage recruitment; chemokine derivative; MCP-1; osteoporosis;
 KW monocyte chemoattractant protein-1; inflammation; atherosclerosis; HIV;

KW	AIDS; stroke; psoriasis; autoimmune disease; hypertension; endotoxaemia;
KM	biosphilm-mediated disease; myocardial infarction; acute ischaemia;
KV	rheumatoid arthritis; contraception; ds.
XX	
OS	Homo sapiens.
XX	
XH	
Key	Location/Qualifiers
FT	CDS 329..628
FT	/tag= a
FT	/product= "human chemokine"
PX	
PN	WO200042071-A2.
XX	
PD	20-JUL-2000.
XX	
PE	12-JAN-2000; 2000WO-US00821.
XX	
PR	12-JAN-1999; 99US-0229071.
PR	17-MAR-1999; 99US-0271192.
PR	01-DEC-1999; .99US-0452406.
XX	
PA	(NEOR-) NEORX CORP.
PI	Grainger DJ, Tatalick LM;
XX	
DR	WPI; 2000-499101/44.
XX	
DR	P-PSDB: AAB15787.
PT	New peptide 3, amide and heterocyclic compounds and saccharide
PT	conjugates used for inhibiting chemokine induced activity and for
PT	treating e.g. stroke, vascular diseases, autoimmune diseases and tumour
PT	growth -
XX	
PS	Disclosure; Page 379-380; 387pp; English.
CC	The present invention concerns the identification of a number of
CC	chemokines which can be used to produce derivatives, agonists and
CC	antagonists which are then useful in treatment. The chemokines
CC	include sequences AAB15785-B15794, AAB15803-B15813 and AAB15831-B15848.
CC	These chemokine derivatives can be used to treat diseases such as
CC	autoimmune diseases, atherosclerosis, osteoporosis, HIV infection and
CC	AIDS, psoriasis, inflammatory diseases, hypertension, basophil-mediated
CC	diseases, endotoxaemia, myocardial infarction, acute ischaemia and
CC	rheumatoid arthritis, and can be used to prevent strokes and as
CC	contraceptives. The chemokine coding sequences AA74858-47488 can be
CC	used in gene therapy for the same diseases, as well as in the production
CC	of animal models.
XX	
SQ	Sequence 1085 BP; 314 A; 214 C; 229 G; 328 T; 0 other:
Query Match	30.1%; Score 257.6; DB 21; Length 1085;
Best Local Similarity	67.9%; Pred. No. 1.5e-42;
Matches 409; Conservative	0; Mismatches 179; Indels 14; Gaps 3,
QY	1 AACCTTACCTCTATGCTGAAGCTCACACCCTTGCCCTCCAAGATGAAGTTCTGCA 60
DB	284 AACCTTCGAATTCTATGTGGAAAGCCATGCCCTCACCCTCGAAGTAAGCCTTGC 343
QY	61 GCGCTTGTCGCTGCTCATGTCAGACCACTTTCAGCCCTCAGAGGAATTGCTGACCA 120
DB	344 GCACCTCTGTGTCTGCTGCTCAGACGACTGTTTCAGAGCCCCAGGGCTTGCTCAGCA 403
QY	121 GATTTCAGTTTCCATTCCAAATCACCTGCTGCTTTAAAGTGATCAATAAGAAAATTCCTATC 180
DB	404 GTTGGGATTAATTAATTCACAATCACTGCTGCTACAGATTATCAATAAAGAAATTCCTTAG 463
QY	181 CAGAGGCTGGAGAGTATACACAAGAATTCACAACATCCAAATGTTCCCAAGAACCTGTGATC 240
DB	464 CAGAGGCTGGAGAGTATACAGAAGGCCACCACTAACCACTGTCCTCCGGAACCTGTAAATC 523
QY	241 TTCAAGACCAAAAGGGGGAAGAGGTCTGTGTGAGACCCCAAGAGAGATGGTCAAGGAT 300
DB	524 TTCAAGACCAAACTGGAAGAGATCTGTGTGTGAGACCCCAAGAGAGATGGTCAAGGAT 583

OY		360	TCCGTGAGACATCGGACCATAATTTCCTGAAGCCATCAGACTTCAATCATGGA
OY		301	
Dd		584	TTTATGAAACAACCTGGACAAAGAAAACCACTCCAAGCTTGGAACATTCAGACTGAA
OY		416	361 CTGAG----AGTCAGACCTTGAAGAAAAGCTTAATTTATTTTCCCACACCTCCAGGTG
OY		703	
Dd		644	CTGAAAAACAAGCCATGACTGAGAACAATTAATTTGTATACCTGTGCCTTCAGAGT
OY		475	417 CAGTGTACATFATTTTTATTATACATCCACAAGA-GATTATTTTTAATAATTTAAAG
OY		763	
Dd		704	GCTTCTCAGATTTATTTTAATCTAATCTAAGATGAGACCTTTATGTATAATGTGAAT
OY		535	476 CATATATTTCTTAAAAAGTATTTAATTAATTAATTTAGTTGTGATGTTTAACCTATCT
Dd		814	
OY		595	764 CATGTTTTTCTTAGTGATTTTAA-----AACTTAATTAATTTAATTTAATCT
OY		874	536 GTCATACATCCTAGTGAATGTAAATGCAAAATCTGGTATGTTGTTTTTGTGTT
OY		874	
OY		874	815 TCATGATTTTGTGGGTTTGTGAACATFAAAGCCTTGATGTATATGTCATCTCAGGCT
OY		876	596 TT 597
Dd		876	875 GT 876
<hr/>			
RESULT 8			
AAA34895			
ID	AAA34895 standard; DNA; 1085 BP.		
XX			
AC	AAA34895;		
XX			
DT	28-JUL-2000 (first entry)		
DE	Human adenosine receptor related polynucleotide SEQ ID NO:2584.		
XX			
KW	Human; adenosine receptor; low adenosine antisense oligonucleotide;		
KM	phosphorothioate; impaired respiration; inflammation; allergy;		
KW	allergic disease; bronchoconstriction; inhibitor; antiinflammatory;		
KM	antiallergic; antiasthmatic; cycostatic; analgesic; impaired airway;		
KW	lung disease; ischememic condition; pulmonary vasoconstriction; asthma;		
KM	respiratory distress syndrome; pain; cystic fibrosis; emphysema;		
KW	pulmonary hypertension; chronic obstructive pulmonary disease; COPD;		
XX	cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.		
OS	Homo sapiens.		
XX			
FN	WO200009525-A2.		
XX			
PD	24-FEB-2000.		
XX			
PF	03-AUG-1999; 99MO-US17712.		
PR	03-AUG-1998; 98US-0095212.		
PA	(UYEC-) UNIV EAST CAROLINA.		
PI	Nyce JW:		
DR	WPI: 2000-205971/18.		
XX			
PT	New antisense oligonucleotides useful for treating e.g. pulmonary		
PT	vasoconstriction, inflammation, allergies, asthma, hypertension,		
PT	bronchitis, emphysema, respiratory distress syndrome, ischemia or		
PT	cancers		
PS	Disclosure; Page 758; 1343pp; English.		
XX			
CC	The present invention describes a new composition comprising an		
CC	antisense oligonucleotide (ON) with low adenosine (up to 15%), which		
CC	targets nucleic acids involved in bronchoconstriction, allergies, and/or		
CC	inflammation. The ON can have antiinflammatory, antiallergic,		
CC	antiasthmatic, cytostatic and analgesic activities. The compositions are		

QY	1	AAACCTTCACCTTCATCTCAAGCTCAACCTTCGCGCTCAAGATGAAGCTTCGCA	60
Db	284	AAACCTTCATCTTCATCTGAGAGCCCACTGCGCTCACCCTCCAAATGAAAGCCTTCGCA	34
QY	61	GCGCTTCGTGCTGCTGCTCATGAGCAGCCACTTTTCAGCCCTCAGAGGACTGTCAGCA	120
Db	344	GCACCTGTGTGCTGCTGCTCAGACGACCTGCTTTCAACCCCGAGGGCTGCTCAGCA	403
QY	121	GATTCAGCTTTCATTCACATCACTGCTGCTTTTAACGATGATCAATGAGAAATTCCTATC	180
Db	404	GTTGGGATTAATTAATCTCAACACTGCTGCTACAGATTATCAATTAAGAAAATCCCTAAG	463
QY	181	CAGAGGCTGGAGAGCTACACAGAATCCAAATCCAAATGCTCCCAAGAGAGTGTGATC	240
Db	464	CAGAGGCTGGAGAGCTACAGAGAGGACACCGACCTGACCTGCTCCCGGAGGCTGTATC	523
QY	241	TTCAAGACCAACGCGGAGAGAGTGTGCTGCTGACCCCAAGAGAGATGGTCAAGGAT	300
Db	524	TTCAAGACCAACGAGAGAGAGATGCTGCTGACCCCAAGAGAGATGGTCAAGGAT	583
QY	301	TTCATGAGCATCTGAGACCAATATTTAAATCTGAAGCATGAGCTTATACATGGA	360
Db	584	TTTATGAGCAGCATGAGACCAAGAAACCCAACTCCAAAGCTTTGAACTATCATGATGA	643
QY	361	CTGAG-----ACGTGAGAGCTGAGAGAAAGCTTATTTTCCCAACCTCCCGCAGGTG	419
Db	644	CTGAGACCAACGAGCATGACTTGGAGAACCAATATTTGATACCTGCTGCTTCACAGT	703
QY	417	CAGTGTGACATTAATTTATTAATCAATCCACAGAGA-GATTATTTTAAATATTTAAG	475
Db	704	GGTCTGAGATTAATTTATTAATCAATTAAGAAATATGAGCTTATGATTAATATGAT	763
QY	476	CATATATTTCTTAAAGTATTTATTAATTTAAGTGTGATGTTTAACTATCT	533
Db	764	CATGTTTCTTAAATATTTAA-----AAGTATTAATTTAATTTAATTTAACT	813
QY	536	GTCATCAATCTGAGATGATAAATGCAAAATCCTGCTGATGATGTTTGTGTTTGT	593
Db	815	TCCATGGAATTTGGTGGTTTGAACATTAAGCCTTGATGATATGATCATCTCAGTCT	873
QY	596	TTT 597	
Db	875	GT 876	

RESULT 10

ABK84649

ABK84649 standard; cDNA: 1085 BP.

ABK84649:

14-AUG-2002 (first entry)

Human cDNA differentially expressed in granulocytic cells #1220.

Human: ss: granulocytic cell; DNA chip: bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.

Homio sapiens.

OS

PN

WO200228999-A2.

11-APR-2002.

PF

03-OCT-2001; 2001WO-US30821.

PR

03-OCT-2000; 2000US-237189P.

PA	(GENE-)	GENE LOGIC INC.
XX	Beazer-Barclay Y,	Weissman SM, Yamaga S, Vockley J;
XX	WPI:	2002-435328/46.
DR		
XX	Detecting granulocyte activation by detecting differential expression	
PT	of genes associated with granulocyte activation, which serves as	
PT	diagnostic markers that is useful for monitoring disease states and	
PT	drug toxicity	
XX		
PS	Claim 1; SEQ ID No 1220; 114pp; English.	
XX		
CC	The invention relates to detecting (M1) granulocyte (GC) activation	
CC	(GCA), by detecting the level of expression of gene(s) (Gs) identified by	
CC	DNA chip analysis as given in the specification, and comparing	
CC	the expression level to an expression level in an unactivated	
CC	GC, where differential expression of Gs is indicative of GCA.	
CC	Also included are modulating (M2) GA by contacting GC with an agent	
CC	that alters the expression of at least one gene in Gs: (2) screening (M3)	
CC	for an agent capable of modulating GCA or an inflammation (especially	
CC	chronic) in a tissue, an allergic response in a subject, exposure of a	
CC	subject to a pathogen or sterile inflammatory disease using the	
CC	gene expression profile; (3) detecting (M4) an inflammation (especially	
CC	chronic) in a tissue, an allergic response in a subject, exposure of a	
CC	subject to a pathogen or sterile inflammatory disease, by detecting the	
CC	level of expression in a sample of the tissue of gene(s) from Gs, where	
CC	the level of expression of the gene is indicative of inflammation;	
CC	(4) treating (M5) an inflammation (especially chronic) or in a tissue,	
CC	an allergic response in a subject, exposure of a subject to a pathogen	
CC	or sterile inflammatory disease, by contacting a tissue having	
CC	inflammation with an agent that modulates the expression of gene(s)	
CC	from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for	
CC	modulating Ga; M3 is useful for screening an agent capable of modulating	
CC	GCA preferably in an inflammation in a tissue; M4 is useful for	
CC	detecting an inflammation (especially chronic) in a tissue, an allergic	
CC	response in a subject, exposure of a subject to a pathogen or sterile	
CC	inflammatory disease (e.g. psoriasis, rheumatoid arthritis,	
CC	glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal	
CC	reperfusion injury, ARDS, adult respiratory distress syndrome,	
CC	inflammatory bowel disease, Crohn's disease, ulcerative colitis,	
CC	periodontal disease; also bacterial infection, viral infection,	
CC	parasitic infection, protozoal infection, fungal infection and M5 is	
CC	useful for treating one of the above conditions. The present	
CC	sequence represents a gene differentially expressed in granulocytes.	
CC	Note: The sequence data for this patent did not form part	
CC	of the printed specification, but was obtained in electronic	
CC	format directly from WIPO at	
CC	ftp.wipo.int/pub/published_pcl_sequences.	
XX		
SQ	Sequence 1085 BP; 314 A; 214 C; 229 G; 328 T; 0 other:	
Query Match	30.1%;	Score 237.6; DB 24; Length 1085;
Best Local Similarity	67.9%;	Pred. No. 1.5e-42;
Matches 409; Conservative	0;	Mismatches 179; Indels 14; Gaps 3
OY	1 AAACCTTCACCCTCATGGTGAAGCGACAACCCCTTCGCCATCAGAATGAAAGTTTCGCA 60	
DB	284 AAACCTTCACATTCATGTATGGGAAGGCCCATGCCCCCTCACCTCCAACATGAAAGCCTTGCA 343	
OY	61 GCGCTTCTGTCGCTCTGCTCATGGCAGCAGCAGCTTTCAGCCCTTCAGAGACTTGGTCAGCCA 120	
DB	344 GCACCTTCTGTGTCTGCTGTGTACAGAGAGCTGCTTAGGCCCCCAGGGGGCTGTGTACGCCA 403	
OY	121 CATTCAGATTTCATTCCAAATCACTGCTGCTTTTAACGTGATCAATAGAAAATTCCTATC 180	
DB	404 GTTGGGATTTAATACATCTCACTACCTGCTCTACAGATTTATCATATAAGAAAAATCCCTAAG 463	
OY	181 CAGAGCGTGAAGCTACACCAAGAAATACCAACATCATATGTGCCAAGAAAGCTGTGATC 240	
DB	464 CAGAGCGTGAAGCTACACCAAGAAAGAACACCAAGTACGCTATCCCGGGGAAGCTGTATATC 523	

KM antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
 KM lung disease; ischemic condition; pulmonary vasoconstriction; asthma;
 KM respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KM pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KM cancer; leukemia; lymphoma; carcinoma; metastasis; ss.
 OS Homo sapiens.
 PN WO200009525-A2.
 PD 24-FEB-2000.
 PF 03-AUG-1999; 99WO-US17712.
 PR 03-AUG-1998; 98US-0095212.
 PA (UYEC-) UNIV EAST CAROLINA.
 PI Nyce JW;
 DR WPI: 2000-205971/18.
 PT New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers -
 PS Disclosure: Page 760-761; 1343pp; English.
 XX The present invention describes a new composition comprising an
 CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
 CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischemic conditions, pulmonary vasoconstriction, allergies,
 CC asthma, impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of
 CC the ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA3213 to AAA5312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
 CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
 CC differ from the previously named sequences. SEQ ID NO:11 to 1680
 CC (AAA3233 to AAA3392) are specifically claimed ONs from the present
 CC invention. N.B. Sequences given in the disclosure of the present
 CC invention do not match up with their corresponding SEQ ID NO: sequences
 CC given in the sequence listing.
 XX
 XX Sequence 5865 BP; 1675 A; 1286 C; 1183 G; 1721 T; 0 other:
 SQ
 Query Match 30.1%; Score 257.6; DB 21; Length 5865;
 Best Local Similarity 67.9%; Pred. No. 2,1e-42;
 Matches 409; Conservative 0; Mismatches 179; Indels 14; Gaps 3;

QY 181 CAGAGCGTGGAGAGCTACACAAGAAATCACCACATCCAAATGTCACGAAGCTGTGATC 240
 DB 1274 CAGAGCGTGGAGAGCTACACAAGAAATCACCACATCCAAATGTCACGAAGCTGTGATC 1333
 QY 241 TTCAGACCAACAGGGGCAAGAGGTGTGCTGACCCCAAGAGAGATGGTCAAGGAT 300
 DB 1334 TTCAGACCAACAGGGGCAAGAGGTGTGCTGACCCCAAGAGAGATGGTCAAGGAT 1393
 QY 301 TCCATGAGACATCTGGACCAATATTTCAAAATCTBAACCCATGACCTTCATACATGGA 360
 DB 1394 TTTATGAGACCACTGGACCAAGAAATCCAACTCCAACTTGAACATTCAGACTGAA 1453
 QY 361 CTGAG----AGTCAGAGCTTGAAGAAAGCTTATTTATTTCCCAACCTCCCCAGGTG 416
 DB 1454 CTGAAACCAAGCCATGACTTGGAGAAAATAATTTGTATACCTGTCTTCTTCAGAGT 1513
 QY 417 CAGTGTACATTTATTTATTTATTAACATCCACAAAGA-GATTATTTTAAATATTTAAAG 475
 DB 1514 GGTTCGAGATTTATTTATTTATTAATCTAATTCGAAGAAATGAGCTTTATGTAATGTAAT 1573
 QY 476 CATATATTTCTTAAATAATATTTATTTATTTAGTGTGATGTTTAACTATATCT 535
 DB 1574 CATGGTTTTCTTAGTAGATTTTAA-----AAGTTATTTAATATTTAATTTAATCT 1624
 QY 536 GTCATACATCTAGTGAATGTAATAATCCCTGGTGTGTTTGTGTTTGT 595
 DB 1625 TCCATGGAATTTGTGGTTTGAACATTAAGCCTTGATGTATATGTCATCTCAGTGCT 1684
 QY 596 TT 597
 DB 1685 GT 1686
 RESULT 14
 AAF21016
 ID AAF21016 standard; DNA; 810 BP.
 AC AAF21016;
 DT 14-MAR-2001 (first entry)
 XX Human low adenosine antisense oligonucleotide related sequence #2583.
 DE
 XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KM human; airway disorder; bronchoconstriction; lung inflammation;
 KM surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KM immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KM respiratory obstruction; pulmonary obstruction; impaired respiration;
 KM surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KM cancer; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200062736-A2.
 PN
 XX 26-OCT-2000.
 PD
 XX
 PF 24-MAR-2000; 2000WO-US08020.
 PR 06-APR-1999; 99US-0127958.
 PA (UYEC-) UNIV EAST CAROLINA.
 PI (NYCE/) NYCE J W.
 XX Nyce JW;
 XX
 XX WPI: 2000-679539/66.
 DR
 PT Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating

PT cancers and respiratory obstructions -
 XX. Disclosure: Page 829; 1592pp; English.
 XX The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antisthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impaired respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention.
 CC
 XX
 SQ Sequence 810 BP; 248 A; 169 C; 155 G; 238 T; 0 other;

Query Match 29.9%; Score 256; DB 21; Length 810;
 Best Local Similarity 67.8%; Pred. No. 3e-42;
 Matches 408; Conservative 0; Mismatches 180; Indels 14; Gaps 3;

QY 1 AAACCTTCACTCTCATGCTGAAGCTACACCTTGCCTCCCAAGATGAAGTTTTCGCA 60
 DB 26 AAACCTTCACTCTCATGCTGAAGCTACACCTTGCCTCCCAAGATGAAGTTTTCGCA 85
 QY 61 GCGCTTCTGCTGCTGCTCATGCGACGACCTTCAGCCCTPAGGAGACTTGTCCGCCA 120
 DB 86 GCGCTTCTGCTGCTGCTCATGCGACGACCTTCAGCCCTPAGGAGACTTGTCCGCCA 145
 QY 121 GATTGAGTTTCCATTCATCACTGCTGCTTAACTGATCAATAGGAATTTCTCATC 180
 DB 146 GTTGGATTAACTTCAACTACCTGCTGCTACAGATTATCAATAAGAAATCCCTAAG 205
 QY 181 CAGAGCTGGAGAGCTACACAAGAAATCACCAATCCATGATGCCAAGAGCTGTGATC 240
 DB 206 CAGAGCTGGAGAGCTACACAAGAAATCACCAATCCATGATGCCAAGAGCTGTGATC 265
 QY 241 TTCAGAGCCAAACGGGGGCAAGAGCTGCTGCTGACCCCAAGAGAGATGGGTCAAGGAT 300
 DB 266 TTCAGAGCCAAACGGGGGCAAGAGCTGCTGCTGACCCCAAGAGAGATGGGTCAAGGAT 325
 QY 301 TCCATGAACCATCTGAGCCAAATATTTCAAAATCTGAAGCATGAGCTTCATACATGCA 360
 DB 326 TTTATGAGACCTGAGCAAGAAACCAAACTCCAAAGCTTTGAAACATTCATGACATGAA 385
 QY 361 CTGA----GAGTCAGAGCTTGAAGAAAGCTTATTTATTTTCCCAACCTCCCCAGGTG 416
 DB 386 CTAAAGAACAGCATGACTTGAAGAAACAATATATTTGTATVACCTGCTTCCTGACAGAT 445
 QY 417 CAGCTGACATTTATTTATTTAATCAATCCCAAGAGAGATTTATTTTAAATTTAAAG 475
 DB 446 GGTTCTGACATTTATTTATTTAATTTCTAAGAAATATGACCTTTATGTAATATGCAAT 505
 QY 476 CATATATTTTCTTAAAGATTTATTTATTTAAGTTGTGATGTTTAACTATATCT 535

DB 506 CATGGTTTTTCTTACTAGATTTTAA-----AACTTATTAATTTTAAATTTACT 556
 QY 536 GTCATACATCCTAGTGAATGTAAATGCAAAATCCTGATGTTTGTGTTTGT 595
 DB 557 TCCATGATTTTGTGGCTTTTGAACATAAAGCTTGAGTATATGTCATCAGTGCT 616
 QY 596 TT 597
 DB 617 GT 618
 RESULT 15
 ID AAA34894
 AAA34894 standard; DNA: 810 BP.
 AC AAA34894;
 XX 28-JUL-2000 (first entry)
 DT
 XX
 DE Human adenosine receptor related polynucleotide SEQ ID NO:2583.
 KW Human: adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antisthmatic; cystostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 OS Homo sapiens.
 XX
 PN W0200009525-A2.
 PD 24-FEB-2000.
 XX
 PF 03-AUG-1999; 99MO-US17712.
 XX
 PR 03-AUG-1998; 98US-0095212.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 PI Nyce JW;
 DR WPI; 2000-205971/18.
 XX
 PT New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers -
 XX
 PS Disclosure: Page 758; 1343pp; English.
 XX
 CC The present invention describes a new composition comprising an
 CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
 CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antisthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
 CC asthma, impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of
 CC the ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 17, 2003, 23:54:35 ; Search time 56 Seconds
(without alignments)
4687.773 Million cell updates/sec

Title: US-10-033-067-2

Perfect score: 856
Sequence: 1 aaacctcactctcatgctc.....actaaaaaaaaaaaaa 856

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_6/prodata/2/lna/5A_COMB.seq:*
2: /cgn2_6/prodata/2/lna/5B_COMB.seq:*
3: /cgn2_6/prodata/2/lna/6A_COMB.seq:*
4: /cgn2_6/prodata/2/lna/6B_COMB.seq:*
5: /cgn2_6/prodata/2/lna/PCUTUS_COMB.seq:*
6: /cgn2_6/prodata/2/lna/backfills1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	256	29.9	814	3	US-07-927-391-15
2	233.2	27.2	605	4	US-09-366-887A-26
3	219.8	25.7	741	3	US-07-927-391-25
4	201	23.5	752	6	5212073-1
5	183.6	21.4	540	4	US-08-744-419-1
6	170.4	19.9	297	4	US-08-613-822-3
7	170.4	19.9	297	4	US-08-852-212-1
8	170.4	19.9	297	4	US-09-479-729B-3
9	170.4	19.9	297	4	US-09-261-201A-3
10	163.2	19.1	315	4	US-08-744-419-3
11	156.8	18.3	994	4	US-09-366-887A-5
12	153.6	17.9	818	4	US-09-366-887A-15
13	139.2	16.3	247	3	US-07-927-391-17
14	138	16.1	228	3	US-07-927-391-13
15	137.4	16.1	228	1	US-08-250-958-3
16	137.4	16.1	231	5	PCr-US95-00605-2
17	96.6	11.3	207	4	US-09-463-458A-28
18	95.2	11.1	207	4	US-09-463-458A-25
19	95.2	11.1	207	4	US-09-463-458A-25
20	91.8	10.7	353	4	US-09-366-887A-21
21	84.2	9.8	151	4	US-09-366-887A-17
22	80.4	9.4	153	4	US-09-366-887A-19
23	76.8	9.0	360	2	US-08-479-126B-1
24	76.8	9.0	360	2	US-08-726-830A-1
25	76.8	9.0	360	3	US-08-995-156A-1
26	76.8	9.0	360	3	US-09-044-856A-1
27	76.8	9.0	360	3	US-09-044-855A-1

28	76.8	9.0	360	4	US-09-419-281-1	Sequence 1, Appl1
29	76.8	9.0	360	5	PCT-US94-05384-1	Sequence 1, Appl1
30	76.8	9.0	360	5	PCT-US96-10087-1	Sequence 1, Appl1
31	72.4	8.5	1235	3	US-08-808-720-8	Sequence 8, Appl1
32	71.8	8.4	737	1	US-08-230-574-3	Sequence 3, Appl1
33	68.6	8.0	99	3	US-07-927-391-12	Sequence 12, Appl1
34	66	7.7	282	2	US-08-535-116-1	Sequence 1, Appl1
35	61.6	7.2	87	3	US-07-927-391-11	Sequence 11, Appl1
36	61.4	7.2	4256	3	US-08-995-156A-21	Sequence 21, Appl1
37	61.4	7.2	4256	4	US-09-419-281-21	Sequence 21, Appl1
38	61.2	7.1	285	3	US-08-995-156A-6	Sequence 6, Appl1
39	61.2	7.1	285	4	US-09-419-281-6	Sequence 6, Appl1
40	60.8	7.1	121	4	US-09-463-458A-4	Sequence 4, Appl1
41	56.6	6.6	117	4	US-09-463-458A-3	Sequence 3, Appl1
42	54.4	6.4	270	1	US-08-208-339A-3	Sequence 3, Appl1
43	54.4	6.4	270	3	US-08-722-719-5	Sequence 5, Appl1
44	53.8	6.3	1234	3	US-08-808-720-6	Sequence 6, Appl1
45	53	6.2	800	1	US-08-230-574-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-07-927-391-15
Sequence 15, Application US/07927391
Patent No. 6001649
GENERAL INFORMATION:
APPLICANT: CAPUT, Daniel
APPLICANT: FERRARA, Pascual
APPLICANT: MILLOUX, Brigitte
APPLICANT: MINY, Adrian
APPLICANT: VITA, Natalio
TITLE OF INVENTION: Protein having a cytokin type
TITLE OF INVENTION: activity, and recombinant DNA, expression vector and hosts
NUMBER OF INVENTION: for its preparation.
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: King Street Station, Suite 500, 1800 Diagonal
STREET: Road, PO Box 299
CITY: ALEXANDRIA
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/927,391
FILING DATE: 19920929
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 16781/369
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 814 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 41..367

```

; FEATURE:
; NAME/KEY: mat-peptide
; LOCATION: 140..367
; FEATURE:
; NAME/KEY: sig-peptide
; LOCATION: 41..139
US-07-927-391-15

```

Query Match	29.9%	Score 256	DB 3	Length 814
Best Local Similarity	67.8%	Pred. No.	5	4e-53
Matches 408	Conservative	0	Mismatches 180	Indels 14
				Gaps 3

QY	1	AAACCTCACCTCTCAGCGTGAAGCTCACACCCCTGGCCCTCCAAAGATGAAGGTTCTGTGA	60
Db	26	AAACCTCAATTCATGCTCATGTGGAAGCCATGCGCCCTCACCTCCAAACATGAAGGCTCTGCA	85
QY	61	GGCGTTTGTGCGCTGCTGCTCATGCGACCCACTTTTACGCGCTTAGGGACTGTGTCAGCCA	120
Db	86	GCACCTTGCTGTCTGCTGCTGCACAGAGCTGTCTTACGCCCCCAGGGGGCTGTGTCAGCCA	145
QY	121	GATTCACGTTTTCATTCCTCAATCACCGTGTGCTTTTAACTGATGATAGAAATATCCATATC	180
Db	146	GTTGGGATTTAATTACTTCAACTACTGCTGCTACAGATTTTCAATTAAGAAAATCCCTAAG	205
QY	181	CAGAGCGTGGAGAGCTACAGAGAAATCCACAGATCCCAATGCTCCCAAGAGAGCTGTGATC	240
Db	206	CAGAGCGTGGAGAGCTACAGAGAACCCAGATAGCCACTGTCCCGGGAGAGCTGTATATC	265
QY	241	TTCAAGACCAACGGGGCCAAAGAGAGTGTGTGCTGACCCCAAGAGAGATGGTCAAGGAT	300
Db	266	TTCAAGACCAAACTGGAGAGAGAGATGTGTGCTGACCCCAAGAGAGTGGGTCAGAGAC	325
QY	301	TTCATGAGACATCTGGAGACCAATTTTCAAAATCTGAAGCATGAGGCTTCATACATGGA	360
Db	326	TTTATGAAGCACTGGAGCAAGAAAACCCAAATCTCAAGAGCTTTGACATTCATGACTGA	385
QY	361	CTGA - - - GAGTCAGAGCTTGAAGAAAAGCTTATTTTCCCAACTCCCCAGGTG	416
Db	386	CTAAAAACAACCCATGACTTGGAGAAACAAATTAATTTGTATACCTGCTCTCCAGAGT	445
QY	417	CAGGTGACATTAATTTATTAATACATCCCAAGA - GATTATTTTAAATATTTAAAG	475
Db	446	GGTCTGAGATTATTTTATCTAATCTTAAGGAATATGACCTTATGTATTAATGTGAAT	505
QY	476	CATAATATTTCTTAAAGAATTAATTAATTAATTAAGTGTGATGTTTAACTCATCT	535
Db	506	CATGCTTTTCTTGTAATTTTAA - - - - - AAGTTATTAATTAATTTAATTTAATCT	556
QY	536	GTCAATACATCTAGTGAATGTAAAGTCAAAATCTGAGTATGTGTTTTGTTTTGTT	595
Db	557	TCCATGAGATTTTGCTGGGTTTTGGAACATAAAGCCTTGAGATGATATGCAATCAGTGCT	616
QY	596	TT 597	
Db	617	GT 618	

RESULT 2
US-09-366-887A-26
Sequence 26, Application US/09366887A
Patent No. 6403782
GENERAL INFORMATION:
APPLICANT: LUSTER, ANDREW D.
APPLICANT: LEDER, PHILIP
APPLICANT: ROTHENBERG, MARC
APPLICANT: GARCIA, EDUADO
TITLE OF INVENTION: EPOXIN: AN EOSINOPHIL
FILE REFERENCE: 00363/025002
CURRENT APPLICATION NUMBER: US/09/366,887A
CURRENT FILING DATE: 1999-08-04
PRIOR APPLICATION NUMBER: 60/000,449
PRIOR FILING DATE: 1995-06-22
PRIOR APPLICATION NUMBER: 08/522,713

```

: PRIOR FILING DATE: 1995-09-01
: PRIOR APPLICATION NUMBER: 08/522,713
: PRIOR FILING DATE: 1998-06-16
: NUMBER OF SEQ ID NOS: 27
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 26
: LENGTH: 605
: TYPE: DNA
: ORGANISM: Mus musculus
US-09-366-887A-26

Query Match      27.2%; Score 233.2; DB 4; Length 605;
Best Local Similarity 69.4%; Pred. No. 1.5e-47;
Matches 379; Conservative 0; Mismatches 155; Indels 14; Gaps 4;

```

QY	1	AAACCTTCACCTCTCAATGCTGAAGGCTACACACCTTGCCCTCCAAAGATGAAGGTTTCTGCA	60
Db	31	AAACCAACCACTCTCAACGCCAAMAGCTACACCTTCAGCCTCCAAACATGAAGGCTCCGCA	90
QY	61	GCAGCTCTGTCGCTGCTGCTCATGGCAGCCATTCACGCCCTCAGGAGCTTCTGCACGCCA	120
Db	91	GCACCTTGATGGGCTGCTGCTCATAGCAGCTCCCTTCAGCCCCCAGGAGGCTCGCTGGGCCA	150
QY	121	GATTCACTTTCCATTCCAAATCACCCTGCTGTTTAACGTATCAATAGAGAAATTTCTATC	180
Db	151	GCTTCTG-----TCCCAACCACTGCTGCTTTAACTGGCCAAATAGGAAGATACCCCTT	204
QY	181	CAGAGGCTGGAGAGCTACACAGAATACCAACATCCATATGTCGCCAAGAGAGCTGTGATC	240
Db	205	CAGGAGCTAGAGACTCTACAGAGATACCAAGTGCCAAATATGTCGCCAAGAAAGCTGTGATC	264
QY	241	TTTCAGACCAAAACGGGGCAGAGAGGTCCTGCTGACCCCAAGAGAGATGGTCAAGGAT	300
Db	265	TTCAAGACCAAACTGGGCCAAGGATATCTGTCGCGACCCCAAGAAAGATGGGTGACGAGAT	324
QY	301	TTCAATGAAGCATCTGGACCAATATTTTCAAATCTGAAGCATGAGCCTTCA--TACATG	358
Db	325	TTCAATGAAGTATCTGGACCAAAATCTCCAACTCAAGACCAATAAATACACCAATTTT	384
QY	359	GACTGAGAGTCAGAGCTTGGAAGAAAGACTATTTATTTCCCAACCTCCCCAGAGTCA	418
Db	385	GAACCAACCAACGAGCCTGAGTGTGCTTATTTGTTTC-----CCTTCTTCAATGCA	439
QY	419	GTCGACATTAATTTTATTAATCAATCCACAAGAGATATTTTAAATTAATTAACCAT	478
Db	440	TTTCGAGGTATCCATTAATCA--GTCCAAAGGCGATGGGTTTATTAATATATATATAT	498
QY	479	AATATTTCTTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	538
Db	499	TTTTTTTTTTTTAAAAAAGCATTTGACATTTAATTAATTAATTAATTAATTAATTAATTAAT	558
QY	539	ATACAT	544
Db	559	CTCCAT	564

```

, RESULT 3
, US-07-927-391-25
, Sequence 25, Application US/07927391
, Patent No. 6001549
, GENERAL INFORMATION:
, APPLICANT: CAPOT, Daniel
, APPLICANT: FERRARA, Pascual
, APPLICANT: MILOUX, Brigitte
, APPLICANT: MINTY, Adrian
, APPLICANT: VITA, Natalio
, TITLE OF INVENTION: Protein having a cytokin type
, TITLE OF INVENTION: activity, and recombinant DNA, expression vector and hosts
, TITLE OF INVENTION: for its preparation.
, NUMBER OF SEQUENCES: 25
, CORRESPONDENCE ADDRESS:
, ADDRESSEE: FOLEY & LARDNER
, STREET: King Street Station, Suite 500, 1800 Diagonal
,

```


NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MIO-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 540 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 56..367
US-08-744-419-1

Query Match 21.4% Score 183.6; DB 4; Length 540;
Best Local Similarity 69.7% Pred. No. 1,4e-35;
Matches 340; Conservative 0; Mismatches 129; Indels 19; Gaps 6;

OY 26 TCACACCCCTTGGCTCCAGAGTGAAGTTCTGCAGCGCTCTGCTGCTGCTCATG 85
DB 36 TCGAGTCTTTCACCTCAACATGAGATTTCACACA---CTTCATGCTCTGCTCATAG 92
OY 86 CAGCACCTTTCAGCCCTCAGGAGTCTGTCAGCCAGATTTCATTTCATTCACATCAGCT 145
DB 93 CTACACACCTTCAGCTCAGTATTGCTGAGACAGATCGGTCGACACCCACGTCACGT 152
OY 146 GGTGTTTAACTGATCATATAGAAATTCCTATCCAGAGCTGGAGAGCTACACAGAA 205
DB 153 GGTGTTTAACTGATCATATAGAAATTCCTATCCAGAGCTGGAGAGCTACACAGAA 212
OY 206 TCACCAACATTCATGATGCTCCAGAGAGTGTATCTTCAGACCAACGAGGAGAGAG 285
DB 213 TCACAGAGCGCCAGAGTGTCCCGGAGAGCTGTATCTTCAGAGACATCTGATAGAGAG 272
OY 266 TCTGTGCTGACCCCAAGAGAGTGGTCAGGATTCATGAAGCATCTGAGACCAATAT 325
DB 273 TCTGTGCTGACCCCAAGAGAGTGGTCAGGATTCATGAAGCATCTGAGATTAAGAGCT 332
OY 326 TTCAAAATTCGAGAGCTGAGCTCATATCATGAGCTGAGAGCAAGCTTGAGAAAG 385
DB 333 CTC-AAACCTTATCTTAACTTATCTTAACTGAGAGCT---TCCAAAAGCTC 385
OY 386 CTATATTTATTTTCCCAACCTCCCGAGGTGAGTGTGACATATTTATTAATCATCC 445
DB 386 TTACGATTTCCCGCGAGAGTTCGCCAGCGGAGGAGTGA---TTTATATGATATCT 441
OY 446 ACAGAGAGATTTATTTTAAATATTTAAAGCATATATTTCTTAAAGATATTTAT 505
DB 442 AAAAGAGAT--GTTTATATATTTAA--ACAAACTGCTTAAATATATTTATATGT 496
OY 506 ATTAACT 513
DB 497 ATTAACT 504

RESULT 6
US-08-613-822-3
Sequence 3, Application US/08613822

Patent No. 6174995
GENERAL INFORMATION:
APPLICANT: Li, Haodong
TITLE OF INVENTION: Human Chemokine Polypeptides
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA

ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/613,822
FILING DATE: 23-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mollstein, Larry S
REGISTRATION NUMBER: 34,679
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8512
TELEFAX: 301-309-8504
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 297 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..294
US-08-613-822-3

Query Match 19.9% Score 170.4; DB 4; Length 297;
Best Local Similarity 75.3% Pred. No. 1,7e-32;
Matches 226; Conservative 0; Mismatches 71; Indels 3; Gaps 1;

OY 46 ATGAGATTTCTCCAGGCTTCTGTGCTCTGCTCATGAGCAGCACTTTCAGCCCTCAG 105
DB 1 ATGAGATTTCTCCAGGCTTCTGTGCTCTGCTCATGAGCAGCACTTTCAGCCCTCAG 60
OY 106 GGAATGCTTACGACATTTAGTTTCATTCATTCATTCATTCATTCATTCATTCATTCAT 165
DB 61 GGAATGCTTACGACATTTAGTTTCATTCATTCATTCATTCATTCATTCATTCATTCAT 120
OY 166 AGCAAAATTCCTATTCAGAGCTGAGAGCTACACAGAAATTCACCAATTCATTCATTCAT 225
DB 121 AAGAAATTCCTATTCAGAGCTGAGAGCTACACAGAAATTCACCAATTCATTCATTCAT 177
OY 226 AAGAAATTCCTATTCAGAGCTGAGAGCTACACAGAAATTCACCAATTCATTCATTCAT 285
DB 178 CAGAGAGCTGCTCATCTTCAGACCAACTGGCAAGAGATCTGTGCTGACCCAAAGAG 237
OY 286 AGATGGTTCAGGATTCATGAGCATCTGACCAATATTTCAAAATTCGAAGCATGA 345
DB 238 AAGTGGTTCAGGATTCATGAGCATCTGACCAATATTTCAAAATTCGAAGCATGA 297

RESULT 7
US-08-852-212-1
Sequence 1, Application US/08852212

Patent No. 6290948
GENERAL INFORMATION:
APPLICANT: White et al.
TITLE OF INVENTION: Method of Treating Sepsis and ARDS using Chemokine Beta-10
FILE REFERENCE: PF501
CURRENT APPLICATION NUMBER: US/08/852,212
CURRENT FILING DATE: 1997-05-06
EARLIER APPLICATION NUMBER: 60/017,871
EARLIER FILING DATE: 1996-05-14
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1

LENGTH: 297
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS


```

; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/744,419
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Provisional
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MIO-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-744-419-3

Query Match      19.1%; Score 163.2; DB 4; Length 315;
Best Local Similarity 72.7%; Pred. No. 9.7e-31;
Matches 224; Conservative 0; Mismatches 83; Indels 1; Gaps 1;

QY 57 TGCAGCCCTTCTGTGCTGTCTGTCATGCGACCCACTTTCAGCCCTCAGGGAGCTGTCTCA 116
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 9  TTCACACTTCTATAGCTCTGCTCATAGTACACCATCGTCTCATGATTTGGCTGG 68
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 117 GCCAGATTCAGTTTCCATTTCATCACCCTGCTGCTTTACGTGATCAATAGAGAAATTC 176
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 69 ACCAGATGCGGTGAGCCACCCAGTACAGTGTATATATGTTTAAAGCAGAGATTC 128
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 177 TATCAGAGGCTGAGAGCTACACAGAAATCCACATCCATGCTCCCAAGAGCTGT 236
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 129 CGTCCGAGAGCTGAGAGCTACAGAGAAATCCACAGAGCCAGTGTCCCGGAAAGCTGT 188
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 237 GATCTTCAGACCAAGGGGAGAGAGTCTGTGCTGACCCCAAGGAGAGATGGGTGAG 296
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 189 GATCTTCAGAGCACTACTGATAGAGATCTGTGCTGACCCCAAGGAGATGGGTGAG 248
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 297 GAATTCATGAGCATGTGAGCACAATATTTCAAAATCTGAAGGCATGAGCCCTTCATCA 356
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 249 GAATTCATTAACCACTTGATAGAGCTGTC-AAACCTTCATCCTTGAACCTTCATGTC 307
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 357 TGGAGCTGA 364
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 308 TAGGCTGA 315

```

```

RESULT 11
US-09-366-887A-5
; Sequence 5, Application US/09366887A
; Patent No. 6403782
; GENERAL INFORMATION:
; APPLICANT: LUSTER, ANDREW D.
; APPLICANT: LEDER, PHILIP
; APPLICANT: ROTHENBERG, MARC
; APPLICANT: GARCIA, EDUARDO
; TITLE OF INVENTION: EOTAXIN: AN EOSINOPHIL CHEMOATTRACTANT
; FILE REFERENCE: 00383/025002
; CURRENT APPLICATION NUMBER: US/09/366,887A
; CURRENT FILING DATE: 1999-08-04
; PRIOR APPLICATION NUMBER: 60/000,449

```

```

; PRIOR FILING DATE: 1995-06-22
; PRIOR APPLICATION NUMBER: 08/522,713
; PRIOR FILING DATE: 1995-09-01
; PRIOR APPLICATION NUMBER: 08/522,713
; PRIOR FILING DATE: 1998-06-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 994
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (35)...(325)
; US-09-366-887A-5

Query Match      18.3%; Score 156.8; DB 4; Length 994;
Best Local Similarity 69.9%; Pred. No. 5.3e-29;
Matches 228; Conservative 0; Mismatches 92; Indels 6; Gaps 1;

QY 22 AAGCTCACACCTTCCTCCAGATGAGGTTTCTGACGCGCTTCTGTGCTGCTC 81
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 11 AACTCCACTCTGTCTCCCTCCACATGACAGAGCTCCACAGCGCTTCTATTCCTGCTGCTC 70
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 82 ATGGCAGCCACTTTAGCCCTCAGGAGCTGCTCAGCCAGATTCAGTTCCATTCCAAATC 141
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 71 ACGGTCACTTCCTTCACTCCAGGTGCTGCTCACCCAGGC-----TCCATCCCAACT 124
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 142 ACCTGCTCTTTAAGCTATCATAGGAAATTCCTATCCAGAGGTGGAGAGCTACACA 201
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 125 TCTGCTGCTTTATATATATACAGTAGAGATGCCCAACACACTACTGAGAGCTTCAAA 184
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 202 AGAATCACCAATCAATGTCCCAAGAGAGCTGTGATCTTCAAGACCAAGGGGCAAG 261
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 185 AGAATCACCAACACAGATGACCTGAAAGCCATAGTCTTCAAGACAGTTGGGCAAA 244
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 262 GAGGTCTGTGACCCCAAGAGATGGTTCAGAGGATTCATGAGCATGTGACCAA 321
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 245 GAGATCTGTGTGACCCCAAGAGAGTGGTTCAGGATGCCAAGACCTGTGACCAA 304
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 322 ATATTCAAAATCTGAGCCATGAGC 347
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 305 AAATCTCAAACTCCAAAACCTAATAC 330

```

```

RESULT 12
US-09-366-887A-15
; Sequence 15, Application US/09366887A
; Patent No. 6403782
; GENERAL INFORMATION:
; APPLICANT: LUSTER, ANDREW D.
; APPLICANT: LEDER, PHILIP
; APPLICANT: ROTHENBERG, MARC
; APPLICANT: GARCIA, EDUARDO
; TITLE OF INVENTION: EOTAXIN: AN EOSINOPHIL CHEMOATTRACTANT
; FILE REFERENCE: 00383/025002
; CURRENT APPLICATION NUMBER: US/09/366,887A
; CURRENT FILING DATE: 1999-08-04
; PRIOR APPLICATION NUMBER: 60/000,449
; PRIOR FILING DATE: 1995-06-22
; PRIOR APPLICATION NUMBER: 08/522,713
; PRIOR FILING DATE: 1995-09-01
; PRIOR APPLICATION NUMBER: 08/522,713
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 818
; TYPE: DNA
; ORGANISM: Guinea pig
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (69)...(356)

```

US-09-366-887A-15

Query Match	17.9%;	Score 153.6;	DB 4;	Length 818;
Best Local Similarity	62.9%;	Pred. No. 2.9e-28;		
Matches 313; Conservative	0;	Mismatches 164;	Indels 21;	Gaps 4

QY	27	CACACCCCTGGCCCTCCCAAGATGAGGGTTTCTGACAGCCCTTGTGGCCGTGCATAGG	86
Db	50	CCCATCTGCACACTGTCACACCATGAAAGTCTCCACAGCCGTTCTGTGCTCTGCTCACA	109
QY	87	AGCCACTTTGAGCCCTCAGGAGACTTGGTCAACCAGATTTCAGTTTCATTCATCAATC	148
Db	110	CTCGCTTTAGGGCCCGCAGTGTCTGGCCATCCAGT-----ATCCCAATGGCTG	160
QY	147	CTGCTTTAACTGTGATCAATAGGAAATTCCTATCCAGAGGCTGAGAGCTACACAGA	206
Db	161	CTGCTTTCGTGTGACCAATAGAGATCTCTTCACAGCACTGAAGAGCTACAAATAT	220
QY	207	CACCAATCCAAATGTGCCAAGGAGCTGTATCTTCAAGACCAACGGGGCAAGAGT	266
Db	221	CACGAGAGCAAAATGTCCCGCAGACGCAATGTCTTTGAGTTCAAACCTGACAAAT	280
QY	267	CTGTGTGACCCCAAGGAGAGTGGGTGACGAGATTTCATGAGCATGTGAGCCAAAT	320
Db	281	ATGTGGCGACCCCAAGAGAGTGGGTTCAGAGTCCCAAGAGTACTGGACCAATATC	340
QY	327	TCAAAATCTGAGGCATGAGCTTCATACATGAGTACGAGATCGAGCTTGAGGAAAGC	386
Db	341	CCAAACTACAAAGCCGTAATC-----ATGTGCTTTAGATGACAAACCGAAATATGCT	394
QY	387	TTATTTATTTCCCAACACTCCGCCAGGTGCAAGTGCATATTTATTTATTAACATCA	446
Db	395	TGATTTATTT-----TCTCTCCTAANAATGATCTCGAATAATATATATAT-TCCCAA	448
QY	447	CAAAAGCATATTTTAAATATTTAAAGCATTAATTTCTTAAAAAGTATTTAATATTA	506
Db	449	AGGGATGACTTTTATTTAAATTTTAAAAAGCAAAATTCATTAAGTTATACAGTCTTA	508
QY	507	TTTAAGTGTGATGTTT 524	
Db	509	AACATATCTTTATGTAT 526	

RESULT 13
 US-07-927-391-17
 Sequence 17, Application US/07927391
 Patent No. 6001649
 GENERAL INFORMATION:
 APPLICANT: CAPUT, Daniel
 APPLICANT: FERRARA, Pascual
 APPLICANT: MILOUX, Brigitte
 APPLICANT: MINY, Adrian
 APPLICANT: VITA, Natalio
 TITLE OF INVENTION: Protein having a cytokin type
 TITLE OF INVENTION: activily and recombinant DNA,expression vector and hosts
 TITLE OF INVENTION: for its preparation.
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FOLEY & LARDNER
 STREET: King Street Station, Suite 500, 1800 Diagonal
 STREET: Road, PO Box 299
 CITY: ALEXANDRIA
 STATE: VIRGINIA
 COUNTRY: USA
 ZIP: 22313-0299
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/927,391
 FILING DATE: 19920929

```

1 CLASSIFICATION: 530
2 ATTORNEY/AGENT INFORMATION:
3 NAME: SAXE, Bernhard D
4 REGISTRATION NUMBER: 28,665
5 REFERENCE/DOCKET NUMBER: 16781/369
6 TELECOMMUNICATION INFORMATION:
7 TELEPHONE: (703) 836-9300
8 TELEFAX: (703) 683-4109
9 TELEX: 899149
10 INFORMATION FOR SEQ ID NO: 17:
11 SEQUENCE CHARACTERISTICS:
12 LENGTH: 247 base pairs
13 TYPE: NUCLEIC ACID
14 STRANDEDNESS: double
15 TOPOLOGY: linear
16 MOLECULE TYPE: DNA (genomic)
17
18 US-07-927-391-17

```

Query Match	16.3%	Score 139.2	DB 3	Length 247
Best Local Similarity	75.0%	Pred. No. 5.5e-25		
Matches: 174	Conservative	0	Mismatches 58	Indels 0
			Gaps	0

OY	115	CAGCAGATTCAGTTCCATTCCATCATCAACCGTGGCTTAACGATGCATGAAGAATAAT	176
Db	16	CAGCCAGTTGGGANTTAATACTTCAACTCTGCTGTCTACGATTTATCAATAAAGAATC	75
OY	175	CCATATCCAGAGCTGGAGAGCTACACAAGAATTCACAACTCATGTCCCAAGAGACT	234
Db	76	CCTAAGCAGAGGCTGGAGAGCTACAGAAGAACCAACGATACCACACTGCCCGGGAAGCT	139
OY	235	GTCATCTTCAAGACCAACGGGGCCAAGGAGGTCTGTGCTGACCCCAAGAGAGATGGTTC	294
Db	136	GTAATCTTCAAGACCAACTGACACAGGAGATCTGTGCTGACCCACACAAAGATGGGTC	195
OY	295	AGGGATTCACAGAACATCTGGACCAATAATTAAAATCTGAAGCATTGAG	346
Db	196	CAGGACTTTATGAAGCACCTGTGACAGAGAAAAACCCAAATCCAAAACCTTTGGAG	247

RESULT 14
 US-07-927-391-13
 : Sequence 13, Application US/07927391
 Patent No. 6001649
 : GENERAL INFORMATION:
 : APPLICANT: CAPUT, Daniel
 : APPLICANT: FERRARA, Pascual
 : APPLICANT: MILLOUX, Brigitte
 : APPLICANT: MINTY, Adrian
 : APPLICANT: VITA, Natalio
 : TITLE OF INVENTION: Protein having a cytokin type
 : TITLE OF INVENTION: activity, and recombinant DNA, expression vector and hosts
 : TITLE OF INVENTION: for its preparation.
 : NUMBER OF SEQUENCES: 25
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: FOLEY & LARDNER
 : STREET: King Street Station, Suite 500, 1800 Diagonal
 : STREET: Road, PO Box 299
 : CITY: ALEXANDRIA
 : STATE: VIRGINIA
 : COUNTRY: USA
 : ZIP: 22313-0299
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/07/927,391
 : FILING DATE: 19920929
 : CLASSIFICATION: 530
 : ATTORNEY/AGENT INFORMATION:
 : NAME: SAYE, Bernhard D
 : REGISTRATION NUMBER: 28,665

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 18, 2003, 03:06:42 ; Search time 70 Seconds
(without alignments)
6228.301 Million cell updates/sec

Title: US-10-033-067-2

Perfect score: 856
Sequence: 1 aaacctcaccctcatgctc.....actaaaaaaaaaaaaa 856

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 424239 seqs, 254661826 residues

Total number of hits satisfying chosen parameters: 848478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA.*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	849	99.2	856	9	US-10-033-067-2
2	842.2	98.4	870	12	US-10-044-090-581
3	841	98.2	2738	8	US-08-927-939-80
4	257.6	30.1	1085	8	US-08-927-939-81
5	244	28.5	256	9	US-10-033-067-7
6	237	27.7	839	8	US-08-927-939-51
7	235.6	27.5	817	12	US-10-044-090-837
8	230.8	27.0	987	12	US-10-044-090-494
9	227.8	26.6	685	8	US-08-927-939-76
10	222.6	26.0	1712	9	US-09-981-876-106
11	222.6	26.0	1712	9	US-09-148-545-105
12	222.6	26.0	1822	9	US-09-981-876-105
13	222.6	26.0	1822	9	US-09-148-545-105
14	221.4	25.9	804	12	US-10-044-090-583
15	218.8	25.6	600	12	US-10-044-090-832
16	216.4	25.3	383	9	US-10-114-893-51
17	213	24.9	236	9	US-10-033-067-5
18	204	23.8	647	10	US-09-777-430A-72
19	203	23.7	825	8	US-08-927-939-28

20	203	23.7	825	8	US-08-927-939-33	Sequence 33, Appl
21	203	23.7	832	12	US-10-044-090-838	Sequence 838, Appl
22	203	23.7	860	10	US-09-872-611A-3	Sequence 3, Appl
23	199.4	23.3	228	9	US-10-033-067-6	Sequence 6, Appl
24	194	22.7	338	9	US-10-040-739-793	Sequence 793, Appl
25	183.4	21.4	289	9	US-10-057-275-1	Sequence 1, Appl
26	170.4	19.9	227	9	US-10-164-621-3	Sequence 3, Appl
27	170.4	19.9	227	9	US-10-125-651-3	Sequence 3, Appl
28	168.8	19.7	297	10	US-09-872-611A-1	Sequence 1, Appl
29	154.8	18.1	258	9	US-09-796-692-7869	Sequence 7869, Ap
30	149.2	17.4	972	9	US-09-792-793A-61	Sequence 61, Appl
31	149.2	17.4	978	9	US-09-792-793A-62	Sequence 62, Appl
32	149.2	17.4	978	9	US-09-792-793A-63	Sequence 63, Appl
33	139	16.2	978	9	US-09-792-793A-52	Sequence 52, Appl
34	139	16.2	984	9	US-09-792-793A-53	Sequence 53, Appl
35	139	16.2	999	9	US-09-792-793A-54	Sequence 54, Appl
36	119.2	13.9	253	10	US-09-833-381-1229	Sequence 1229, Ap
37	110.4	12.9	453	10	US-09-864-761-1789	Sequence 1789, Ap
38	104.4	12.2	476	10	US-09-864-761-5570	Sequence 5570, Ap
39	102.2	11.9	400	10	US-09-833-381-1234	Sequence 1234, Ap
40	99.8	11.7	724	12	US-10-044-090-839	Sequence 839, Appl
41	93.8	11.0	231	9	US-09-792-793A-67	Sequence 67, Appl
42	93.8	11.0	978	9	US-09-792-793A-55	Sequence 55, Appl
43	93.8	11.0	984	9	US-09-792-793A-56	Sequence 56, Appl
44	93.8	11.0	999	9	US-09-792-793A-57	Sequence 57, Appl
45	79.6	9.3	360	10	US-09-864-761-5454	Sequence 5454, Ap

ALIGNMENTS

```
RESULT 1
US-10-033-067-2
; Sequence 2, Application US/10033067
; Patent No. US20020164704A1
; GENERAL INFORMATION:
; APPLICANT: Coleman, Roger
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: NOVEL HUMAN MONOCYTE CHEMOTACTIC PROTEIN
; FILE REFERENCE: PF-0069-1 CON
; CURRENT APPLICATION NUMBER: US/10/033,067
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 08/683,655
; PRIOR FILING DATE: 1996-07-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 856
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte ID No. US20020164704A1 965517CB1
; NAME/KEY: unsure
; LOCATION: 628, 650, 653, 676, 769, 779, 820
; OTHER INFORMATION: a, t, c, g, or other
US-10-033-067-2

Query Match          99.2% ; Score 849; DB 9; Length 856;
Best Local Similarity 100.0% ; Pred. No. 1.9e-147;
Matches 856; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 AAACCTCACCCTGCATGCAAGCTCACACCCCTGCCCTCAGATGCAAGCTTCTGCA 60
DB 1 AAACCTCACCCTGCATGCAAGCTCACACCCCTGCCCTCAGATGCAAGCTTCTGCA 60
QY 61 GCGCTTGTCGCGCTGCTCATGCGACGACCTTACAGCCCTCAGGACCTTGCACGCA 120
DB 61 GCGCTTGTCGCGCTGCTCATGCGACGACCTTACAGCCCTCAGGACCTTGCACGCA 120
QY 121 GATTCACTTCCATCCATCACCCTGCTTAAAGTGAATAGCAAAATTCCTATC 180

DB 121 GATTGAGTTTCATTCCAAATCACTGCTGCTTTTAACTGATCAATGAGAAATTCCTTANC 180
QY 181 CAGAGGCTGAGAGCTACCAAGAAATCACCACATCCATGTCCTCCAGGAGGCTGATC 240
DB 181 CAGAGGCTGAGAGCTACCAAGAAATCACCACATCCATGTCCTCCAGGAGGCTGATC 240
QY 241 TTCAGAGCCAAACGGGGCAGAGAGCTGTGCTGACCCCAAGAGAGATGGGTGAGGAT 300
DB 241 TTCAGAGCCAAACGGGGCAGAGAGCTGTGCTGACCCCAAGAGAGATGGGTGAGGAT 300
QY 301 TCCATGAGACATCTGAGCCAAATATTTCAAATCTGAAGCCATGAGCTTCATATGGA 360
DB 301 TCCATGAGACATCTGAGCCAAATATTTCAAATCTGAAGCCATGAGCTTCATATGGA 360
QY 361 CTGAGAGCTGAGAGCTGAGAGAAAGCTTATTTATTTCCCAACCTCCCCAGGTGAT 420
DB 361 CTGAGAGCTGAGAGCTGAGAGAAAGCTTATTTATTTCCCAACCTCCCCAGGTGAT 420
QY 421 GTGACATTTATTTATTAATCAATCCAAAGAGATTTATTTAAATTTAAAGCATTA 480
DB 421 GTGACATTTATTTATTAATCAATCCAAAGAGATTTATTTAAATTTAAAGCATTA 480
QY 481 TATTTCTTAAAAAGTATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 540
DB 481 TATTTCTTAAAAAGTATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 540
QY 541 ACATCTAGTGAATGTAATGCAAAATCCTGCTGATGCTGCTGCTGCTGCTGCTGCT 600
DB 541 ACATCTAGTGAATGTAATGCAAAATCCTGCTGATGCTGCTGCTGCTGCTGCTGCT 600
QY 601 GTGAGCTCAACTAGTCAAGTCCGCAAAANGTCAATGCTGCTGCTGCTGCTGCTGCT 660
DB 601 GTGAGCTCAACTAGTCAAGTCCGCAAAANGTCAATGCTGCTGCTGCTGCTGCTGCT 660
QY 661 TTGTGGGCTCCTCCCTGATCATCAAGTGAAGCACTAGTATCTTGGCAATCAGT 720
DB 661 TTGTGGGCTCCTCCCTGATCATCAAGTGAAGCACTAGTATCTTGGCAATCAGT 720
QY 721 GCTCCTGTAAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
DB 721 GCTCCTGTAAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
QY 781 TAACATGGAATTTGAAAAAATTTCAAAAAAGAAANATATATATTTAAACATTA 840
DB 781 TAACATGGAATTTGAAAAAATTTCAAAAAAGAAANATATATATTTAAACATTA 840
QY 841 AAAAAAAAAAAAAA 856
DB 841 AAAAAAAAAAAAAA 856

RESULT 2
US-10-044-090-581
; Sequence 581, Application US/10044090
; Patent No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044, 090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 581
; LENGTH: 870
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 2883526CB1
US-10-044-090-581

Query Match 98.4%; Score 842.2; DB 12; Length 870;

Best Local Similarity 98.8%; Pred. No. 3,3e-146;
Matches 844; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 AAACCTTACCTTCTATGCTGAAAGCTCACACCTTGGCTCCCAAGATGAAGGTTTCTGCA 60
DB 17 AAACCTTACCTTCTATGCTGAAAGCTCACACCTTGGCTCCCAAGATGAAGGTTTCTGCA 76
QY 61 GGGCTTGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 77 GGGCTTGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 136
QY 121 GATTGAGTTTCATTCCAAATCACTGCTGCTTTTAACTGATCAATGAGAAATTCCTTANC 180
DB 137 GATTGAGTTTCATTCCAAATCACTGCTGCTTTTAACTGATCAATGAGAAATTCCTTANC 196
QY 181 CAGAGGCTGAGAGCTACCAAGAAATCACCACATCCATGTCCTCCAGGAGGCTGATC 240
DB 197 CAGAGGCTGAGAGCTACCAAGAAATCACCACATCCATGTCCTCCAGGAGGCTGATC 256
QY 241 TTCAGAGCCAAACGGGGCAGAGAGCTGTGCTGACCCCAAGAGAGATGGGTGAGGAT 300
DB 257 TTCAGAGCCAAACGGGGCAGAGAGCTGTGCTGACCCCAAGAGAGATGGGTGAGGAT 316
QY 301 TCCATGAGACATCTGAGCCAAATATTTCAAATCTGAAGCCATGAGCTTCATATGGA 360
DB 317 TCCATGAGACATCTGAGCCAAATATTTCAAATCTGAAGCCATGAGCTTCATATGGA 376
QY 361 CTGAGAGCTGAGAGCTGAGAGAAAGCTTATTTATTTCCCAACCTCCCCAGGTGAT 420
DB 377 CTGAGAGCTGAGAGCTGAGAGAAAGCTTATTTATTTCCCAACCTCCCCAGGTGAT 436
QY 421 GTGACATTTATTTATTAATCAATCCAAAGAGATTTATTTAAATTTAAAGCATTA 480
DB 437 GTGACATTTATTTATTAATCAATCCAAAGAGATTTATTTAAATTTAAAGCATTA 496
QY 481 TATTTCTTAAAAAGTATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 540
DB 497 TATTTCTTAAAAAGTATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 556
QY 541 ACATCTAGTGAATGTAATGCAAAATCCTGCTGATGCTGCTGCTGCTGCTGCTGCT 600
DB 557 ACATCTAGTGAATGTAATGCAAAATCCTGCTGATGCTGCTGCTGCTGCTGCTGCT 616
QY 601 GTGAGCTCAACTAGTCAAGTCCGCAAAANGTCAATGCTGCTGCTGCTGCTGCTGCT 660
DB 617 GTGAGCTCAACTAGTCAAGTCCGCAAAANGTCAATGCTGCTGCTGCTGCTGCTGCT 676
QY 661 TTGTGGGCTCCTCCCTGATCATCAAGTGAAGCACTAGTATCTTGGCAATCAGT 720
DB 677 TTGTGGGCTCCTCCCTGATCATCAAGTGAAGCACTAGTATCTTGGCAATCAGT 736
QY 721 GCTCCTGTAAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
DB 737 GCTCCTGTAAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 796
QY 781 TAACATGGAATTTGAAAAAATTTCAAAAAAGAAANATATATATTTAAACATTA 840
DB 797 TAACATGGAATTTGAAAAAATTTCAAAAAAGAAANATATATATTTAAACATTA 856
QY 841 AAAAAAAAAAAAAA 854
DB 857 AAAAAAAAAAAAAA 870

RESULT 3
US-08-927-939-80
; Sequence 80, Application US/08927939
; Patent No. US2001006640A1
; GENERAL INFORMATION:
; APPLICANT: Grainger, David J.
; APPLICANT: Tatalick, Lauren Marie
; TITLE OF INVENTION: Compounds and methods to inhibit or
; TITLE OF INVENTION: augment an inflammatory response.

```

; FILE REFERENCE: 295.022US1
; CURRENT APPLICATION NUMBER: US/08/927,939
; CURRENT FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 2738
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (123)...(353)
; US-08-927-939-80

```

Query Match 98.2%; Score 841; DB 8; Length 2738;

Best Local Similarity 98.6%; Pred. No. 7e-146;

Matches 844; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

```

OY 1 AACCTTCACCTCTCATGCTGAAGCTCACACCTTGCCCTCCCAAGATGAAGTTCTGCA 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 12 AACCTTCACCTCTCATGCTGAAGCTCACACCTTGCCCTCCCAAGATGAAGTTCTGCA 71
OY 61 GGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 72 GGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 131
OY 121 GATTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 132 GATTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 191
OY 181 CAGAGCTGAGAGCTACACACACACACACACACACACACACACACACACACACACAC 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 192 CAGAGCTGAGAGCTACACACACACACACACACACACACACACACACACACACACAC 251
OY 241 TTCACACACACACACACACACACACACACACACACACACACACACACACACACACAC 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 252 TTCACACACACACACACACACACACACACACACACACACACACACACACACACACAC 311
OY 301 TCCATGACATCTGACCAATATTTCAAAATCTGAAGCATGAGCTTCATCATGGA 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 312 TCCATGACATCTGACCAATATTTCAAAATCTGAAGCATGAGCTTCATCATGGA 371
OY 361 CTGAGAGCTGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 372 CTGAGAGCTGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 431
OY 421 GTGACATATTTTATTAATACATCCACAAAGAGATTTTAAATATTTAAAGCATAA 480
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 432 GTGACATATTTTATTAATACATCCACAAAGAGATTTTAAATATTTAAAGCATAA 491
OY 481 TATTTCTTAAAAAGTATTTATTAATATTTAAGTTGTTAAGTTTAACTGATCTGCAT 540
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 492 TATTTCTTAAAAAGTATTTATTAATATTTAAGTTGTTAAGTTTAACTGATCTGCAT 551
OY 541 ACATCTAGATGATGAATAATGCAAAATCTGGATGATGTTTCTTTTCTTTTCTTCT 600
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 552 ACATCTAGATGATGAATAATGCAAAATCTGGATGATGTTTCTTTTCTTTTCTTCT 611
OY 601 GTGAGCTCACTAAGTTACAGGCCCAAAAGTCAATGTTCTCCCTCCACGCTGCTAGTG 660
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 612 GTGAGCTCACTAAGTTACAGGCCCAAAAGTCAATGTTCTCCCTCCACGCTGCTAGTG 671
OY 661 TTGTGGGGTCTCCCTGATGATCATCAAGGTGAACACTTGAAGTATTTTGGCATAGT 720
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 672 TTGTGGGGTCTCCCTGATGATCATCAAGGTGAACACTTGAAGTATTTTGGCATAGT 731
OY 721 GCTCCCTAGTGAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 732 GCTCCCTAGTGAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 791
OY 781 TAACATGCAATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 792 TAACATGCAATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 851

```

```

OY 841 AAAAAAAAAAAAAA 856
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 852 AAAAAAAAAAAAAA 867

```

RESULT 4

US-08-927-939-81

; Sequence 81, Application US/08927939

; Patent No. US20010006640A1

; GENERAL INFORMATION:

; APPLICANT: Grainger, David J.

; APPLICANT: Tatalick, Lauren Marie

; TITLE OF INVENTION: Compounds and methods to inhibit or

; FILE REFERENCE: 295.022US1

; CURRENT APPLICATION NUMBER: US/08/927,939

; CURRENT FILING DATE: 1997-09-11

; NUMBER OF SEQ ID NOS: 83

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 81

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (329)...(625)

US-08-927-939-81

Query Match

Best Local Similarity 30.1%; Score 257.6; DB 8; Length 1085;

Matches 409; Conservative 0; Mismatches 179; Indels 14; Gaps 3;

```

OY 1 AACCTTCACCTCTCATGCTGAAGCTCACACCTTGCCCTCCCAAGATGAAGTTCTGCA 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 284 AACCTTCACCTCTCATGCTGAAGCTCACACCTTGCCCTCCCAAGATGAAGTTCTGCA 343
OY 61 GGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 344 GGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 403
OY 121 GATTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 404 GATTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 463
OY 464 CAGAGCTGAGAGCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 523
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 524 CAGAGCTGAGAGCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 583
OY 584 TTTATGAAGCAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 643
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 644 TTTATGAAGCAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 703
OY 644 CTGAGAGCAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 703
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 703 CTGAGAGCAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 703
OY 704 GCTTCTGAGATTTTATTAATCTTAATCTTAATCTTAATCTTAATCTTAATCTTAAT 763
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 764 GCTTCTGAGATTTTATTAATCTTAATCTTAATCTTAATCTTAATCTTAATCTTAAT 814
OY 815 GCTATACCTAGTGAATGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 874
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 874 GCTATACCTAGTGAATGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG

```


Query Match	27.5%;	Score 235.6;	DB 12;	Length 817;
Best Local Similarity	67.7%;	Pred. No. 6.9e-35;		
Matches 409; Conservative	0;	Mismatches 179;	Indels 16;	Gaps 5;

OY	1	AAACCTTCACCTCTCATGTCGAAGGCTTACACACCCCTGGCCCTCCCAAGATGAAGTTCCT	-GC	59
Db	26	AAACCTCCATTCATTCATGTCGAAAGCCCATGCGCCCTCACCTCCCAACATGAAGCCTCGGC		85
OY	60	AGCGCTTCGTGCCT -GCTGCTCATGGCAGCCACCTTCAGCCCTCAGGAGCTTGCTAGC		118
Db	86	AGCACTTCGTGTCGTGCTCTCACACACACTGCTTTCACGCCCCAGGGCCTTGCTAGC		145
OY	119	CAGATTAGTTTCATTCCATACCTCGCTGCTTTAACCGATCAATAGSAAAAATTCCTA		178
Db	146	CAGTTGGATTAACTACTTCAACTACCTGGCGCTACACATTTATCAATAAAGAAATCCCTA		205
OY	179	TCCAGAGGCTGAGAGGCTTACACAAGATCCACAATGCATGCCAAGGAAGCTGTGA		238
Db	206	AGCAGAGGCTGAGAGGCTTACAGAAGACCAACAGTACCACTGTCCCCGGGAAGCTGTAA		265
OY	239	TCTTCAAGACCAACGGGGCAGAGAGTCTGTGCTGACCCCAAGAGAGATGGGTCAGGG		298
Db	266	TCTTCAAGACCAACCTGGACAGAGATCTGTGCTGACCCACACACAACTGGGCTCCAGG		325
OY	299	ATTCATGAAGACATCTGACCAAAATATTTCATAATCGAAGCCATGAGGCTTCATACATG		358
Db	326	ACTTTATGAAGCACTCTGACACAGAAACCCAAACTCCAAAGCTTTGAACTTCATGTACTG		385
OY	359	GACTGAG ---AGTCAGAGCTTGAGAGAAAGCTATTATTATTTTCCCAACCTCCCCAGG		414
Db	386	AACGTGAAGAACGACCATGACTGTGGAAGAACAAATTAATTGATACCGTGCTTTCCTGAGA		445
OY	415	TGCAAGTGTGACATTATTTATTATACATCCACAAAGA -GATTAATTTTAAATATTTAA		473
Db	446	GTCGTTCTGAGATTTATTTTATCTAACTCAAGGAATATAGCTTTATGTAAATATCTGA		505
OY	474	AGCATTAATATTCTTAAAGATATTATATTATTAAAGTGTGAGATTTTAACTCAT		533
Db	506	ATCATGGTTTTTCTTAGTACATTTAA -----AAGTTATTAATATTTTAATTTTAAT		556
OY	534	CTGTGATACATCTAGTGAATGTAAAAATGCAAAATCCTGGTATGATGTTTTGTTTTG		593
Db	557	CTTCCATGAGATTTTGTGGGGCTTTGAACATAAAGCCTTGATGTATATGTCACTCAGTG		616
OY	594	TTTTT 597		
Db	617	CTGT 620		

```

RESULT 8
US-10-044-090-494
; Sequence 494, Application US/10044090
; Patent No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044,090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 494
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 222839.1
US-10-044-090-494

```

Query Match	27.0%;	Score 230.8;	DB 12;	Length 9877
Best Local Similarity	68.0%;	Pred. No. 5.5e-34;		

Matches 400; Conservative 0; Mismatches 172; Indels 16; Gaps 5;

OY	1	AAACCTTCACCTGTCATGCGTGAAGGCTCACACCCCTGGCCCTCCAAAGATGAAGGTTTTCGA	60
Db	159	AAACCCACCACTCTCAGCGCAAGGCTTACACCTTCACCTCCCAACATGAAGGTTCTCCGA	218
OY	61	GCCTCTGTGCGCGTGTGCATGCGACGACATTTTCAGCCCTCAGGAGACTTGGTCAAGCCA	120
Db	219	GCACTTCTGTGGCGTGCCTCATAGCAGCTGGCCCTCAGGCCCAAGGGCGCTCACTGGGCCA	278
OY	121	GATTCACTTCCATTCCTCAATCACCTGCTGCTTTTACGTGATCANTATGAAAATTCCTATC	180
Db	279	GCTTCTG-----TCCCAACCACTGCTGCTTTTAACTGGCCATATGGAAGATACCCCTT	332
OY	181	CAGGSGTGGAGACTCCACAAGATACCAACATCCAAATGTCGCCAAGAGAGCTGTGATC	240
Db	333	CAGGACTAGAGACTCTACAGAGATACCAAGTGCCAAATGTCCCAAGAAAGCTGTGATC	332
OY	241	TTTCAGACCAAAACGGGGCAGAGAGAGTGTGCTGACCCCAAGAGAGATGGGTCAAGGAT	300
Db	393	TTCAAGACCAAACTGGGCGCAAGATATCTGTGGCGAGCCCAAGAAAGATGGGTGCAAGAT	452
OY	301	TTCCATGAAGCATCTGGACCAATATTTCAAAATCTGAAGCCATGAGCCTTCATCATG--	358
Db	453	TTCCATGAAGATCTGGACCAAAATCTCCAACTCCAAAGCCATAAATACACCATTTT	512
OY	359	GACGAGAGTCAGAGCTTGAAGAAAGACCTATTTATTTCCCAACCTCCCCAGGCGCA	418
Db	513	GAACCAACCAACGAGGCGCTGAGTGTGGCTATATTTGTTTC-----CCTTCTTACAAATGCA	567
OY	419	GTCGACATTATTTATTTATACATCCACCAAGAGATTTATTTAAATTAATTTAAAGCAT	478
Db	568	TTTCAGAGTAACTCCATTAAT--CAGTCCAAAGGGCAGGGTTTATTAATATATATATA	625
OY	479	AATATTTCTTAAAGATTAATTAATTAATTAAGTGTGATGTTTAACTC-TATCTGT	537
Db	626	TTTTTTTTTAAAAAAGAGTATGCTTAATTAATTTATGAGGCTTTAAAAACTTATCTC	685
OY	538	CATACATCTCAGATGAATGAATAAAGCAAAATCCGAGATGATGTTTT	585
Db	686	CATAAATATCTAGTATATTTTAAACGTGAAGCTTTGGCAGATTCCTT	733

```

RESULT 9
US-08-927-939-76
: Sequence 76, Application US/08927939
: Patent No. US2001000640A1
: GENERAL INFORMATION:
: APPLICANT: Gralinger, David J.
: APPLICANT: Tatallick, Lauren Marie
: TITLE OF INVENTION: Compounds and methods to inhibit or
: TITLE OF INVENTION: augment an inflammatory response.
: FILE REFERENCE: 295.022051
: CURRENT APPLICATION NUMBER: US/08/927,939
: CURRENT FILING DATE: 1997-09-11
: NUMBER OF SEQ ID NOS: 83
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 76
: LENGTH: 661
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (32)...(331)
: US-08-927-939-76

```

Query Match	26.6%	Score 227.8	DB 8	Length 685
Best Local Similarity	53.8%	Pred. No. 1.8e-33		
Matches 370; Conservative	9	Mismatches 196	Indels 3	Gaps 3

Qy 14 TCATGCTGAAGCTCACACCCTTCGCCCTCCAAAGATGAAGTTTCTGCACGGCCTTGCGCC 73
||| |||||||| ||| || |||||| |
Db 1 TCAACTGAGACTCGCACTTCGCC -TCAGCATGAAGAATCTCTGCCGCCCTTGTGTGCC 59


```

P R I O R F I L I N G D A T E : 1997-08-22
P R I O R A P P L I C A T I O N N U M B E R : 60/056, 909
P R I O R F I L I N G D A T E : 1997-08-22
P R I O R A P P L I C A T I O N N U M B E R : 60/056, 875
P R I O R F I L I N G D A T E : 1997-08-22
P R I O R A P P L I C A T I O N N U M B E R : 60/056, 862
P R I O R F I L I N G D A T E : 1997-08-22
P R I O R A P P L I C A T I O N N U M B E R : 60/056, 887
P R I O R F I L I N G D A T E : 1997-08-22
P R I O R A P P L I C A T I O N N U M B E R : 60/056, 908
P R I O R F I L I N G D A T E : 1997-08-22
P R I O R A P P L I C A T I O N N U M B E R : 60/048, 964
P R I O R F I L I N G D A T E : 1997-06-06
P R I O R A P P L I C A T I O N N U M B E R : 60/057, 650
P R I O R F I L I N G D A T E : 1997-09-05
P R I O R A P P L I C A T I O N N U M B E R : 60/056, 884
P R I O R F I L I N G D A T E : 1997-08-22
N U M B E R O F S E Q I D N O S : 280
S O F T W A R E : Patentln Ver. 2.0
S E Q I D N O 106
L E N G T H : 1712

Query Match      26.0%; Score 222.6; DB 9; Length 1712;
Best Local Similarity 68.3%; Pred. No. 2e-32;
Matches 405; Conservative 1; Mismatches 160; Indels 27; Gaps 6;

QY      1  A A A C C T T C A C C T C T C A T G C T G A A G C T C A C A C C C T T G C C C T C C A A G A T G A A G G T T T C G C A 60
DB      946  A A A C C C A A T T C T C A A A C T G A A G C T G C A C T C T G C - C C T C A G C A T G A A A G T C T C T G C C 1004

QY      61  G C G C T T C T G T G C C T G C T G C T C A T G G C A G C C A C T T T C A G C C C T C A G G A C A C T T G C T C A G C C A 120
DB      1005  G C C C C T T G T G C C G C G C T C T C A T A G C A G C A C C A C C T T C A T T C C C C A A G G C C T G C T C A G C C A 1064

QY      121  G A T T C A G T T T C C A T T C C A A T C C A T C C T G C G C T T T A A C G T G A T C A A T A G A A A A T T C T A T C 180
DB      1065  G A T C A C A T C A A T G C C C C A G T A C C T G C T G T A T A C T T A C C A A T A G A A G A T C T C A G T G 1124

QY      181  C A G A G C C T G A G A G C T A C A C A A G A A T C A C A A C A T T C C A A T G C C C A A G A A G C T G T G A T C 240
DB      1125  C A G A G C C T G C G A C C T A T A G A A A A T C A C C A G C A G A A G T G T C C C A A A G A A G C T G T G A T C 1184

QY      241  T T C A A G A C C A A C G G G C A G A G A G T C T G T C T A C C C C A A G A G A G A T G G G T C A G G A T 300
DB      1185  T T C A A G A C C A T T G T G C C A A G A G A T C T G T C T A C C C C A A G C A A G A A T G G G T T C A G A T 1244

QY      301  T C C A T G A A G C A T C T G G A C C A A T A T T T C A A A T C T G A A G C C A T G A G C C T C A T A C A T G A 360
DB      1245  T C C A T G G C A C C T G G A C A A C C A A C C A A C C C A A G A A T T T G A A C A C T A C T C A C A C A 1304

QY      361  C T G A G A C T A G A G C T T G A A A A A G C T A T T A T T A T T T T C C C A C A C C T C C C C A G G T G C A G T 420
DB      1305  C C C A - - - - A A A A C T G A G A G T A A - - - - C T A T T T T T C C C T A G C T T T C C C A G A C A C C C T 1355

QY      421  G T G C A T A T T A T T A T T A T A C A T C C A C A A G A G A T A T T T T T A A A T A A T T T T A A A G C A T A A 480
DB      1356  G T T T A T T A T T A T T A T A T - - - - - - - - - - G A A T T T G T T G T G A T G A A A C A T - - 1399

QY      481  T A T T T C T A A A A A G A T A T T A T A T T A T T A T T A G T G T G A T G A T T T T A A C T A C T A C A T C A T G C A T 540
DB      1400  T A T C C C T A A A G T A A T G T A A T C T T A T T A T T A G T A T G A T A T T T T A A G T A A G T T A T C T T C A T 1459

QY      541  A C A T C C T A G T A A A T G T A A A A T G C A A A A T C C G T G A T G A T G T T T T T T G T T T T G 593
DB      1460  G G - T A C T A G T G T T T T T A G A T A C A G A G A C T T G G G A A A T T G C T T T C C T C T G 1511

RESULT 11
US-09-148-545-106
; Sequence 106, Application US/09148545
; Publication No. US20030027132A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

```

TITLE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: P2001P1
CURRENT APPLICATION NUMBER: US/09/148,545
EARLIER FILING DATE: 1998-09-04
EARLIER APPLICATION NUMBER: PCT/US98/04482
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,161
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,336
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,163
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,597
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,502
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,633
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,583
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,617
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,618
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,503
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,592
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,581
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,584
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,500
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,587
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,492
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,598
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,613
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,582
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,596
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,612
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,632
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,601
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,580
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,568
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,314
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,569
EARLIER FILING DATE: 1997-04-11

```
;; EARLIER APPLICATION NUMBER: 60/047,585
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,586
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,590
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,594
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,589
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,593
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/047,614
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/043,578
;; EARLIER FILING DATE: 1997-04-11
;; EARLIER APPLICATION NUMBER: 60/043,576
;; EARLIER FILING DATE: 1997-04-11
;; EARLIER APPLICATION NUMBER: 60/047,501
;; EARLIER FILING DATE: 1997-05-23
;; EARLIER APPLICATION NUMBER: 60/043,670
;; EARLIER FILING DATE: 1997-04-11
;; EARLIER APPLICATION NUMBER: 60/056,632
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/056,664
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/056,876
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/056,881
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/056,909
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/056,875
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/056,862
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/056,887
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/056,908
;; EARLIER FILING DATE: 1997-08-22
;; EARLIER APPLICATION NUMBER: 60/048,964
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/057,650
;; EARLIER FILING DATE: 1997-09-05
;; EARLIER APPLICATION NUMBER: 60/056,884
;; EARLIER FILING DATE: 1997-08-22
;; NUMBER OF SEQ ID NOS: 280
;; SOFTWARE: Patentln Ver. 2.0
;; SEQ ID NO 106
;; LENGTH: 1712
```

```
Query Match      26.0%; Score 222.6; DB 9; Length 1712;
Best Local Similarity 68.3%; Pred. No. 2e-32;
Matches 405; Conservative 1; Mismatches 160; Indels 27; Gaps 6;

OY 1 AACCTTCACCTCATGCTGAAGCTCACACCCCTTGCCCTCCCAAGATGAAGTTTTCGCA 60
Db 946 AACATTCATTCCTCAACTGAAGCTGACCTCG-CTCCGACGATGAAGTCTCGCC 1004
OY 61 GCGCTTCGCTGCTGCTCATGAGCAGCCTTTCAGCCCTCAGGAGCTGCTCAGACCA 120
Db 1005 GCGCTTCGCTGCTGCTCATGAGCAGCAGCCTTTCATTTCCCAAGGCTCGCTCAGCCA 1064
OY 121 GATTCAGTTTCATTCACATCACTGCTCTTAACTGATCAATAGAAATTCCTATC 180
Db 1065 GATTCAGTTTCATTCACATCACTGCTCTTAACTGATCAATAGAAATTCCTATC 1124
OY 181 CAGAGGCTGAGAGCTACACAGAAATCACCACATCAATGTCCTCCAGAGAGCTGATC 240
Db 1125 CAGAGGCTGAGAGCTATGAGAAATCACCAGAGCAAGTGTCCCAAGAGCTGATC 1184
OY 241 TTCAGAGCCAAAGGGGCAAGGAGCTGTGCTGAGCCCAAGAGAGATGGCTCAGGAT 300
Db 1185 TTCAGAGCCATTTGGCCCAAGGAGATCTGCTGACCCCAAGCAGAAAGTGGCTCAGAT 1244
```

```
Db 301 TCCATGAGAGCTGAGCAACCAATATTTCAAAATGAGAGCCATGAGCCTTCATCATGGA 360
OY 1245 TCCATGAGAGCAACCTGAGCAACCAACCAATTCGAAAGATTTGAGACCTCAGCTCAGAA 1304
OY 361 CTGAGAGCTCAGAGCTTGAAGAAAGCTTATTTATTTTCCCAACCTCCCAAGGTGACAT 420
Db 1305 CCCA-----AGAACTCAGCTAA-----CTTATTTTCCCTAGCTTCCCAAGACACCT 1355
OY 421 GTGACATTATTTTATTAACATCCACAAGATTTATTTTAATATTTAAAGCATTA 480
Db 1356 GTTTATTTATTTATTAAT-----GAATTTTGTGTTGATGGAACAT-- 1399
OY 481 TATTTCTTAAAGATTTATTTATTTATTTAGTTGATGTTTAACTATCTGTCAT 540
Db 1400 TATTCCTTAAATGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1459
OY 541 ACATCTGAGTGAATGTAATGCAAAATCTGTGATGCTTTTGTGTTTGT 593
Db 1460 GG-TACTAGCTTTTATTAAGATACAGAGACTGGGGAATTCCTTTCTCTTG 1511

RESULT 12
US-09-981-876-105
; Sequence 105, Application US/09981876
; Patent No. US2002016469A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2001P1
; CURRENT APPLICATION NUMBER: US/09/981,876
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/148,545
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,161
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,615
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,600
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,597
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,502
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,633
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,583
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,617
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,618
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,503
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,592
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,581
; PRIOR FILING DATE: 1997-05-23
```

PRIOR APPLICATION NUMBER: 60/047,584
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,500
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,587
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,492
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,598
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,613
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,582
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,596
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,612
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,632
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,601
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/043,580
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,568
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,314
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,569
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,311
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,671
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,674
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,669
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,312
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,313
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,672
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,315
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/048,974
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/056,886
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,877
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,889
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,893
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,630
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,878
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,662
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,872
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,882
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,637
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,903
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,888
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,879

```

; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 105
; LENGTH: 1822

```

Query Match	26.0%;	Score 222.6;	DB 9,	Length 1822;
Best Local Similarity	68.3%;	Pred. No. 2e-32;		
Matches 405; Conservative	1;	Mismatches 160;	Indels 27;	Gaps 6

QY	1	AAACCTTCACCTCTCAATGCGAAGCTCACACCTTGTGCTCCCTCCAAAGTGTGAAGTTCTGTGA	60
Db	1056	AAACATTCATTTCTCAACTGAAAGCTCGACCTGCG-CTCCAGCATGAAAGTCTCTGCG	111
QY	61	GCGCTCTGTGCTGCTGCTCATGGCAGCCATTTGAGCCCTCAGGAGACTTGCTCAGCCA	120
Db	1115	GCCCTCTGTGCTGCTGCTCATAGAGCCACTTTCATTTCCCAAGGCGTCCGTACGCCA	117
QY	121	GATTCATTTTCCATTCATTCACCTGCTGTTAACGTGATCAATGGAATAATTCTCTATC	180
Db	1175	GATTCAAATCAATGCCCGACCTGCTCTGTATTAACCTTACCAATGTGAAGATCTCAGTG	123
QY	181	CAGAGCTGGAGAGCTCACAGAATACCAATCCATTCATGTCGCCAAGAGACTGTGATC	240
Db	1235	CAGAGCTCCCGAGCTTTAAGAAATACACAGCAGCAAGTGTCCCAAGAAAGCTGTGATC	129
QY	241	TTCAAGACCAAGCGGGCAAGGAGGTGTGCTGACCCCAAGAGAGATGGGTCAAGGAT	300
Db	1295	TTCAAGACCAATTTGTGGCCAGAGAGATCTGTGCTGACCCCAAGAGAGTGGGTTCAGAT	135
QY	301	TTCCATGAAGATCTGGAACCAATATTTCAAAATCTGAAGCCATGAGCCTTCATACATGGA	360
Db	1355	TTCAATGACCACTGGACCAAGCAACCCCAACCTCGAAGACTTGAACACTCTACCTCACAA	141
QY	361	CTGAGAGTCAAGCTTGAAGAAAGCTTATTATTTTCCCAACCTCCGCCAGGTGCAAT	420
Db	1415	CCCA-----AGAACTGCGACTAA-----CTTATTTTCCCTTACCTTTCCCGACACCTT	146
QY	421	GTCGACATTTATTTATTTATAACATCCACAAGAGATTATTTTAAATATTTTAAAGCATAA	480
Db	1466	GTTTATTTTATTTATTAAT-----CAATTTGTGTTGTTGATGTAACAAT--	150
QY	481	TATTTCTAAAAAGTATTATTAATATTATTAAGTGTGTGATGTTTAACTCTATCTGTCAAT	540
Db	1510	TATCCCTTAAGTATGTTATTTCTTAAATTAAGTATTGATGTTTAAAGTTATCTTTTCAT	156
QY	541	ACATCTAGAGAAATGTAATGCAAAATCGTGTGATGCTTTTGTGTTTGG 593	
Db	1570	GG-TACTAGAGTTTTTATGATTAACGAGACTTGGGGAAATGCTTTTCCCTTGG 1621	

```

RESULT 13
US-09-148-545-105
? Sequence 105, Application US/09148545
? Publication No. US20030027132A1
? GENERAL INFORMATION:
?   APPLICANT: Rosen et al
?   TITLE OF INVENTION: 70 Human Secreted Proteins
?   FILE REFERENCE: P2001P1
?   CURRENT APPLICATION NUMBER: US/09/148,545
?   CURRENT FILING DATE: 1998-09-04
?   EARLIER APPLICATION NUMBER: PCT/US98/04482
?   EARLIER FILING DATE: 1998-03-06
?   EARLIER APPLICATION NUMBER: 60/040,162
?   EARLIER FILING DATE: 1997-03-07
?   EARLIER APPLICATION NUMBER: 60/040,333
?   EARLIER FILING DATE: 1997-03-07
?   EARLIER APPLICATION NUMBER: 60/038,621
?   EARLIER FILING DATE: 1997-03-07
?   EARLIER APPLICATION NUMBER: 60/040,161
?   EARLIER FILING DATE: 1997-03-07
?   EARLIER APPLICATION NUMBER: 60/040,626

```

1	EARLIER	FILING DATE:	1997-03-07
2	EARLIER	APPLICATION NUMBER:	60/040,334
3	EARLIER	FILING DATE:	1997-03-07
4	EARLIER	APPLICATION NUMBER:	60/040,336
5	EARLIER	FILING DATE:	1997-03-07
6	EARLIER	APPLICATION NUMBER:	60/040,163
7	EARLIER	FILING DATE:	1997-03-07
8	EARLIER	APPLICATION NUMBER:	60/047,615
9	EARLIER	FILING DATE:	1997-05-23
10	EARLIER	APPLICATION NUMBER:	60/047,600
11	EARLIER	FILING DATE:	1997-05-23
12	EARLIER	APPLICATION NUMBER:	60/047,597
13	EARLIER	FILING DATE:	1997-05-23
14	EARLIER	APPLICATION NUMBER:	60/047,502
15	EARLIER	FILING DATE:	1997-05-23
16	EARLIER	APPLICATION NUMBER:	60/047,618
17	EARLIER	FILING DATE:	1997-05-23
18	EARLIER	APPLICATION NUMBER:	60/047,503
19	EARLIER	FILING DATE:	1997-05-23
20	EARLIER	APPLICATION NUMBER:	60/047,592
21	EARLIER	FILING DATE:	1997-05-23
22	EARLIER	APPLICATION NUMBER:	60/047,581
23	EARLIER	FILING DATE:	1997-05-23
24	EARLIER	APPLICATION NUMBER:	60/047,584
25	EARLIER	FILING DATE:	1997-05-23
26	EARLIER	APPLICATION NUMBER:	60/047,500
27	EARLIER	FILING DATE:	1997-05-23
28	EARLIER	APPLICATION NUMBER:	60/047,588
29	EARLIER	FILING DATE:	1997-05-23
30	EARLIER	APPLICATION NUMBER:	60/047,492
31	EARLIER	FILING DATE:	1997-05-23
32	EARLIER	APPLICATION NUMBER:	60/047,598
33	EARLIER	FILING DATE:	1997-05-23
34	EARLIER	APPLICATION NUMBER:	60/047,613
35	EARLIER	FILING DATE:	1997-05-23
36	EARLIER	APPLICATION NUMBER:	60/047,582
37	EARLIER	FILING DATE:	1997-05-23
38	EARLIER	APPLICATION NUMBER:	60/047,596
39	EARLIER	FILING DATE:	1997-05-23
40	EARLIER	APPLICATION NUMBER:	60/047,612
41	EARLIER	FILING DATE:	1997-05-23
42	EARLIER	APPLICATION NUMBER:	60/047,632
43	EARLIER	FILING DATE:	1997-05-23
44	EARLIER	APPLICATION NUMBER:	60/047,601
45	EARLIER	FILING DATE:	1997-04-11
46	EARLIER	APPLICATION NUMBER:	60/043,560
47	EARLIER	FILING DATE:	1997-04-11
48	EARLIER	APPLICATION NUMBER:	60/043,568
49	EARLIER	FILING DATE:	1997-04-11
50	EARLIER	APPLICATION NUMBER:	60/043,314
51	EARLIER	FILING DATE:	1997-04-11
52	EARLIER	APPLICATION NUMBER:	60/043,569
53	EARLIER	FILING DATE:	1997-04-11
54	EARLIER	APPLICATION NUMBER:	60/043,669
55	EARLIER	FILING DATE:	1997-04-11
56	EARLIER	APPLICATION NUMBER:	60/043,312
57	EARLIER	FILING DATE:	1997-04-11
58	EARLIER	APPLICATION NUMBER:	60/043,313
59	EARLIER	FILING DATE:	1997-04-11
60	EARLIER	APPLICATION NUMBER:	60/043,672
61	EARLIER	FILING DATE:	1997-04-11

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 18, 2003, 01:54:36 ; Search time 69 Seconds
(without alignments)
6318.566 Million cell updates/sec

Title: US-10-033-067-2
Perfect score: 856
Sequence: 1 aaacctcactctcatgct.....actaaaaaaaaaaaaa 856

Scoring table: IDENTITY_NMC
Gapop 10.0 , Gapext 1.0

Searched: 424239 seqs, 254661826 residues

Total number of hits satisfying chosen parameters: 848478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	849	99.2	856	9 US-10-033-067-2	Sequence 2, Appli
2	842.2	98.4	870	12 US-10-044-090-581	Sequence 561, App
3	841	98.2	2738	8 US-08-927-939-80	Sequence 80, Appl
4	257.6	30.1	1085	8 US-08-927-939-81	Sequence 81, Appl
5	244	28.5	256	9 US-10-033-067-7	Sequence 7, Appli
6	237	27.7	839	8 US-08-927-939-51	Sequence 51, Appl
7	235.6	27.5	817	12 US-10-044-090-837	Sequence 837, App
8	230.8	27.0	987	12 US-10-044-090-494	Sequence 494, App
9	227.8	26.6	685	8 US-08-927-939-76	Sequence 76, Appl
10	222.6	26.0	1712	9 US-09-981-876-106	Sequence 106, App
11	222.6	26.0	1712	9 US-09-148-545-106	Sequence 106, App
12	222.6	26.0	1822	9 US-09-981-876-105	Sequence 105, App
13	222.6	26.0	1822	9 US-09-148-545-105	Sequence 105, App
14	221.4	25.9	804	12 US-10-044-090-583	Sequence 823, App
15	218.8	25.6	600	12 US-10-044-090-822	Sequence 822, App
16	216.4	25.3	383	9 US-10-114-893-51	Sequence 51, Appl
17	213	24.9	236	9 US-10-033-067-5	Sequence 5, Appli
18	204	23.8	647	10 US-09-777-430A-72	Sequence 72, Appl
19	203	23.7	825	8 US-08-927-939-28	Sequence 28, Appl

20	203	23.7	825	8 US-08-927-939-33	Sequence 33, Appl
21	203	23.7	832	12 US-10-044-090-838	Sequence 838, App
22	203	23.7	860	10 US-09-872-611A-3	Sequence 3, Appli
23	199.4	23.3	328	9 US-10-033-067-6	Sequence 6, Appli
24	194	22.7	338	9 US-10-040-739-793	Sequence 793, App
25	183.4	21.4	289	9 US-10-057-275-1	Sequence 1, Appli
26	170.4	19.9	297	9 US-10-164-621-3	Sequence 3, Appli
27	170.4	19.9	297	9 US-10-125-451-3	Sequence 3, Appli
28	168.8	19.7	297	10 US-09-872-611A-1	Sequence 1, Appli
29	154.8	18.1	258	9 US-09-796-697-7869	Sequence 7869, App
30	149.2	17.4	972	9 US-09-792-793A-61	Sequence 61, Appl
31	149.2	17.4	978	9 US-09-792-793A-62	Sequence 62, Appl
32	149.2	17.4	993	9 US-09-792-793A-63	Sequence 63, Appl
33	139	16.2	984	9 US-09-792-793A-52	Sequence 52, Appl
34	139	16.2	984	9 US-09-792-793A-53	Sequence 53, Appl
35	139	16.2	999	9 US-09-792-793A-54	Sequence 54, Appl
36	119.2	13.9	253	10 US-09-833-381-1229	Sequence 1229, App
37	110.4	12.9	453	10 US-09-864-761-1789	Sequence 1789, App
38	104.4	12.2	476	10 US-09-864-761-5570	Sequence 5570, App
39	102.2	11.9	400	10 US-09-833-381-1234	Sequence 1234, App
40	99.8	11.7	724	12 US-10-044-090-839	Sequence 839, App
41	93.8	11.0	231	9 US-09-792-793A-67	Sequence 67, Appl
42	93.8	11.0	978	9 US-09-792-793A-55	Sequence 55, Appl
43	93.8	11.0	984	9 US-09-792-793A-56	Sequence 56, Appl
44	93.8	11.0	999	9 US-09-792-793A-57	Sequence 57, Appl
45	79.6	9.3	360	10 US-09-864-761-5454	Sequence 5454, App

ALIGNMENTS

RESULT 1
US-10-033-067-2
; Sequence 2, Application US/10033067
; Patent No. US20020164704A1
; GENERAL INFORMATION:
; APPLICANT: Coleman, Roger
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: NOVEL HUMAN MONOCYTE CHEMOTACTIC PROTEIN
; FILE REFERENCE: PF-0069-1 CON
; CURRENT APPLICATION NUMBER: US/10/033,067
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 08/683,655
; PRIOR FILING DATE: 1996-07-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 856
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020164704A1 965517CBI
; NAME/KEY: unsure
; OTHER INFORMATION: a, t, c, g, or other
; US-10-033-067-2

Query Match 99.2% Score 849; DB 9; Length 856;
Best Local Similarity 100.0%; Pred. No. 1.9e-147;
Matches 856; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AAACCTTCACCTCTCATGCTGAAGCTACACCCCTTCCTCAAGATGAAGCTTCTGCA	60
DB	1	AAACCTTCACCTCTCATGCTGAAGCTACACCCCTTCCTCAAGATGAAGCTTCTGCA	60
QY	61	GGCGTTCTGCTGCTGCTCATGCGACGACCTTTAGCCCTCAGGAGCTTGTCAGCCA	120
DB	61	GGCGTTCTGCTGCTGCTCATGCGACGACGACCTTTAGCCCTCAGGAGCTTGTCAGCCA	120
QY	121	GATTCACTTTCATTCATTCACCTGCTGCTTTAACGTATGAGAAATTCCTATC	180

D	b	121	GATTCACTTTCCATTCCTCAATCCACTGCTGCTTAAAGCTGATCTAATAGGAAAATTCCTATC	180
Q	y	181	CAGAGCGTGAAGAGACTACACAAGAATTCACACATCCATCCATGTCCTCCAAGAGAGCTGTGATC	240
D	b	181	CAGAGCGTGAAGAGACTACACAAGAATTCACACATCCATCCATGTCCTCCAAGAGAGCTGTGATC	240
Q	y	241	TTCCAAAGCCAAACCGGGCAGAAGAGTCTGTGCTGACCCCAAGAGAGATGGGTCAAGGAT	300
D	b	241	TTCCAAAGCCAAACCGGGCAGAAGAGTCTGTGCTGACCCCAAGAGAGATGGGTCAAGGAT	300
Q	y	301	TCCATTAAGCATCTGAGACCAAAATATTTCCAAAATCTGAAAGCATGAGACCTTCATACATGA	360
D	b	301	TCCATTAAGCATCTGAGACCAAAATATTTCCAAAATCTGAAAGCATGAGACCTTCATACATGA	360
Q	y	361	CTGAGAGTCAGAGCTTGAAAGAAAAGCTTATTTATTTTCCCAACCTCCCCAGGTGCAGT	420
D	b	361	CTGAGAGTCAGAGCTTGAAAGAAAAGCTTATTTATTTTCCCAACCTCCCCAGGTGCAGT	420
Q	y	421	GTGACATTTATTTATTTATTAACATCCACAAGAGATTTATTTTAAATATTTTAAAGCATAA	480
D	b	421	GTGACATTTATTTATTTATTAACATCCACAAGAGATTTATTTTAAATATTTTAAAGCATAA	480
Q	y	481	TATATCTAAAAAGTATTTATTTATTTATTTAAGTGTGATGTTTAACTATACCTGCTCAT	540
D	b	481	TATATCTAAAAAGTATTTATTTATTTATTTAAGTGTGATGTTTAACTATACCTGCTCAT	540
Q	y	541	ACATCTAGAGTAAGTAAATATGCAAAATCCGTGATGTGTTTTGTTTTGTTTTTCCCT	600
D	b	541	ACATCTAGAGTAAGTAAATATGCAAAATCCGTGATGTGTTTTGTTTTGTTTTTCCCT	600
Q	y	601	GTGAGCTCAACTAAAGTTCACGGCCAAANGTCATATTTGTTCTCCCTCAACNGTNCGTAGTG	660
D	b	601	GTGAGCTCAACTAAAGTTCACGGCCAAANGTCATATTTGTTCTCCCTCAACNGTNCGTAGTG	660
Q	y	661	TTTGGGGGTCTCCCNNGATCATCAAGGTGAACACTTGAAGTATCTTTGGCAATCAGT	720
D	b	661	TTTGGGGGTCTCCCNNGATCATCAAGGTGAACACTTGAAGTATCTTTGGCAATCAGT	720
Q	y	721	GCTCTCTGAAGTCAAAAGTGTGCTTGTACTGCTGTGTGAATGANGTACTGTANA	780
D	b	721	GCTCTCTGAAGTCAAAAGTGTGCTTGTACTGCTGTGTGAATGANGTACTGTANA	780
Q	y	781	TAACTATGGAATTTTGAAAAAAAAAATTCAAAAACAAAAANATATATTAATTTAAAACTA	840
D	b	781	TAACTATGGAATTTTGAAAAAAAAAATTCAAAAACAAAAANATATATTAATTTAAAACTA	840
Q	y	841	AAAAAAAAAAAAAAAAAAAA 856	
D	b	841	AAAAAAAAAAAAAAAAAAAA 856	

```

RESULT 2
US-10-044-090-581
; Sequence 581 Application US/10044090
; Patent No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044, 090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO: 581
; LENGTH: 870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID NO. US20020137081A1 2883526CBI
US-10-044-090-581

```

Query Match 98.48; Score 842.2; DB 12; Length 870;

Best Local Similarity	.98.88;	Pred. No. 3.3e-16;
Matches	844;	Conservative 0; Mismatches 10; Indels 0; Gaps 0;

[illegible]

RESULT 3
 US-08-927-939-80
 ; Sequence 80, Application US/08927939
 ; Patent No US2010006640A1
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Gralinger, David J.
 ; APPLICANT: Gralinger, Lauren Marie
 ; TITLE OF INVENTION: Compounds and methods to inhibit or
 ; TITLE OF INVENTION: augment an inflammatory response.

FILE REFERENCE: 295.022US1
 : CURRENT APPLICATION NUMBER: US/08/927,939
 : CURRENT FILING DATE: 1997-09-11
 : NUMBER OF SEQ ID NOS: 83
 : SOFTWARE: FastSeq for Windows Version 3.0
 : SEQ ID NO: 80
 : LENGTH: 2738
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: (123)...(353)
 : US-08-927-939-80

Query Match 98.2%; Score 841; DB 8; Length 2738;
 Best Local Similarity 98.6%; Pred. No. 7e-146;
 Matches 844; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 1 AAACCTTCACCTCTCATGCTGAAGCTCACACCCCTGCCCTCAAGATGAAGTTTCTGCA 60
 DB 12 AAACCTTCACCTCTCATGCTGAAGCTCACACCCCTGCCCTCAAGATGAAGTTTCTGCA 71
 OY 61 GCGCTTCGTGCTGCTGCTCATGAGCCACTTTCAGCCCTCAGGAGACTTGTGACCCA 120
 DB 72 GCGCTTCGTGCTGCTGCTCATGAGCCACTTTCAGCCCTCAGGAGACTTGTGACCCA 131
 OY 121 GATTCAGTTTCCATTCATCAATCACTGCTCTTAAAGTGAATAGAAATTTCCATAC 180
 DB 132 GATTCAGTTTCCATTCATCAATCACTGCTCTTAAAGTGAATAGAAATTTCCATAC 191
 OY 181 CAGAGGCTGAGAGCTACACAGAAATCACCACATCCATGTCCTCCAGAGAGCTGTGATC 240
 DB 192 CAGAGGCTGAGAGCTACACAGAAATCACCACATCCATGTCCTCCAGAGAGCTGTGATC 251
 OY 241 TTCAGAGCAACAGGGGCGAGAGAGGTGCTGAGCCCAAGAGAGAGATGGTCAGGAT 300
 DB 252 TTCAGAGCAACAGGGGCGAGAGAGGTGCTGAGCCCAAGAGAGAGATGGTCAGGAT 311
 OY 301 TCCATGAAGCATCTGAGCAAAATATTTCAAAATCTGAAGCATGACCTTCAATACATGA 360
 DB 312 TCCATGAAGCATCTGAGCAAAATATTTCAAAATCTGAAGCATGACCTTCAATACATGA 371
 OY 361 CTGAGAGTCAGAGCTTGAGAAAGAGCTTATTTATTTTCCCAACCTCCAGAGTGCAGT 420
 DB 372 CTGAGAGTCAGAGCTTGAGAAAGAGCTTATTTATTTTCCCAACCTCCAGAGTGCAGT 431
 OY 421 GTGACATTTTATATATATCAATCCACAAAGAGATTTTAAATATTTAAAGCTAA 480
 DB 432 GTGACATTTTATATATATCAATCCACAAAGAGATTTTAAATATTTAAAGCTAA 491
 OY 481 TATTTCTTAAAGATTTTAAATATTTTAAAGTGTGATGTTTAACTATCTGTCAT 540
 DB 492 TATTTCTTAAAGATTTTAAATATTTTAAAGTGTGATGTTTAACTATCTGTCAT 551
 OY 541 ACATCTAGTGAATGAATGCAAAATCTGCTGATGTTTATTTTGTGTTTCTTCT 600
 DB 552 ACATCTAGTGAATGAATGCAAAATCTGCTGATGTTTATTTTGTGTTTCTTCT 611
 OY 601 GTGAGCTCAACTAAGTTCACGGCCAAANGTCATGTTTCTCCCTACACGTCAGTATG 660
 DB 612 GTGAGCTCAACTAAGTTCACGGCCAAANGTCATGTTTCTCCCTACACGTCAGTATG 671
 OY 661 TTGTTGGGCTCTCCCTGATCATCAAGGGAAGCACTTATGTTTGGCAATCAGT 720
 DB 672 TTGTTGGGCTCTCCCTGATCATCAAGGGAAGCACTTATGTTTGGCAATCAGT 731
 OY 721 GCTCTGTAAGTCAATGTGTGCTTTGTAAGTGTGTTGTAATGANGTCTACTGTANA 780
 DB 732 GCTCTGTAAGTCAATGTGTGCTTTGTAAGTGTGTTGTAATGANGTCTACTGTANA 791
 OY 781 TAACTATGAATTTTGAAGAAATTTTCAAGAAAGAAANATATATATATTTAAACTA 840
 DB 792 TAACTATGAATTTTGAAGAAATTTTCAAGAAAGAAANATATATATATTTAAACTA 851

OY 841 AAAAAAAAAAAAAA 856
 DB 852 AGAAAAAAAAAAAAA 867

RESULT 4

US-08-927-939-81
 : Sequence 81, Application US/08927939
 : Patent No. US2001006640A1
 : GENERAL INFORMATION:
 : APPLICANT: Grainger, David J.
 : APPLICANT: Tatalick, Lauren Marie
 : TITLE OF INVENTION: Compounds and methods to inhibit or
 : FILE REFERENCE: 295.022US1
 : CURRENT APPLICATION NUMBER: US/08/927,939
 : CURRENT FILING DATE: 1997-09-11
 : NUMBER OF SEQ ID NOS: 83
 : SOFTWARE: FastSeq for Windows Version 3.0
 : SEQ ID NO: 81
 : LENGTH: 1085
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: (329)...(625)
 : US-08-927-939-81

Query Match 30.1%; Score 257.6; DB 8; Length 1085;
 Best Local Similarity 67.9%; Pred. No. 6.8e-39;
 Matches 409; Conservative 0; Mismatches 179; Indels 14; Gaps 3;

OY 1 AAACCTTCACCTCTCATGCTGAAGCTCACACCCCTGCCCTCAAGATGAAGTTTCTGCA 60
 DB 284 AAACCTTCACCTCTCATGCTGAAGCTCACACCCCTGCCCTCAAGATGAAGTTTCTGCA 343
 OY 61 GCGCTTCGTGCTGCTGCTCATGAGCCACTTTCAGCCCTCAGGAGACTTGTGACCCA 120
 DB 344 GCGCTTCGTGCTGCTGCTCATGAGCCACTTTCAGCCCTCAGGAGACTTGTGACCCA 403
 OY 121 GATTCAGTTTCCATTCATCAATCACTGCTCTTAAAGTGAATAGAAATTTCCATAC 180
 DB 404 GATTCAGTTTCCATTCATCAATCACTGCTCTTAAAGTGAATAGAAATTTCCATAC 463
 OY 181 CAGAGGCTGAGAGCTACACAGAAATCACCACATCCATGTCCTCCAGAGAGCTGTGATC 240
 DB 464 CAGAGGCTGAGAGCTACACAGAAATCACCACATCCATGTCCTCCAGAGAGCTGTGATC 523
 OY 241 TTCAGAGCAACAGGGGCGAGAGAGGTGCTGAGCCCAAGAGAGAGATGGTCAGGAT 300
 DB 524 TTCAGAGCAACAGGGGCGAGAGAGGTGCTGAGCCCAAGAGAGAGATGGTCAGGAT 583
 OY 301 TCCATGAAGCATCTGAGCAAAATATTTCAAAATCTGAAGCATGACCTTCAATACATGA 360
 DB 584 TCCATGAAGCATCTGAGCAAAATATTTCAAAATCTGAAGCATGACCTTCAATACATGA 643
 OY 361 CTGAG----AGTCAAGCTTGAAGAAAGCTTATTTTCCCAACCTCCAGAGTGC 416
 DB 644 CTGAGAAACAGCCATGACTGAGAAACAAATATTTGATACCTGCTCTTCTGCAAGT 703
 OY 417 CAGTGTACATTTATTTATATACATCACAAAGA--GATATTTTAAATATTTAAAG 475
 DB 704 GGTTCAGATTTATTTATATATTTCTAAGAGATATGAGCTTTATGTAATATGTAAT 763
 OY 476 CATTAATTTCTTAAAGATTTTAAATATTTTAAAGTGTGAGTTTAACTATCTATCT 535
 DB 764 CATGTTTCTTAAAGATTTTAA-----AAGTTATTAATATTTTAAATATCT 814
 OY 536 GTCATATCTCTAGTGAATGTAATGCAAAATCTGCTGATGTTTGTGTTTGT 595
 DB 815 TCCATGATTTTGTGTTTGAACATTAAGCCCTGAGTATATGTCATCATCTAGTCT 874

Matches	400, Conservative	0, Mismatches	172, Indels	16, Gaps	5
1	AAACCTTCACCTCTCATGCTGAAGCTCACACCCCTGCCCTCAAGTGAAGTTTGTGCA	60			
100					
150					
200					
250					
300					
350					
400					
450					
500					
550					
600					
650					
700					
750					
800					
850					
900					
950					
1000					

QY	1	AAACCTTCACCTCTCAGCTGAAAGCTACACACCTTGCCCTCCAAAGATGAAGGTTTTCGA	60
Db	159	AAACACACACCTCTCAGAGCCAAAGCTCACACCTTCAGCCTTCAACATGAAAGTCTCGCA	218
QY	61	GGCCTCTGACCTGCTGCTCATGAGCCACCTTCACGCTTCAGGACCTTGCTCAACCA	120
Db	219	GCATCTCTTGAGGCTGCTGCTCATAGCAGCTGCTTACGCCCCAGGGGCTCACTGGGCCA	278
QY	121	GATTCACCTTTCACATCCCAATCACCTGGCTTAAAGCTGATCAATAGGAATATTCATC	180
Db	279	GCTTCTG-----TCCCAACACCTGCTGCTTTAACTGGCCAAATAGGAATATCCCTT	332
QY	181	CAGAGCCTGAGAGCTACACAGAATCCACACATCCAAATGTCGCCAAGAGAGCTGTGATC	240
Db	333	CAGGAGCTAGAGAGCTACAGGAAGATCACCAGTGGCAAAATGTCCCCAGAAAGCTGTATC	392
QY	241	TTCAAGACCAACGGGGCCAAAGAGTCTGTGCTGACCCCAAGAGAGATGGCTCAGGAT	300
Db	393	TTCAAGACCAAACTGGCCAAAGAGATCTGTGCCGACCCCAAGAAAGTGGGTGCAGGAT	452
QY	301	TTCCATGAGACATCGAGACCAAAATTTTCCAAATCTGAAGCATGAGCCTCATACATC--	358
Db	453	TTCCATGAGAGTATCGAGACCAAAATTTTCCAAATCTGAAGCATGAGCCTCATACATTTT	512
QY	359	GACGGAAGTCAGAGCTTGAAGAAAGAACTTATTTATTTTCCCAACCTCCCCAGAGTGA	418
Db	513	GAACCAACCAAGAGCCTGAGTGTGGCTTAATTTGTTTC-----CCTTCTTACAAATGCA	567
QY	419	GTCGTGACATTATTTTATTTATPAACATCCACAAAGAGATTATTTTAAATTAATTPAAGCAT	478
Db	568	TTTCGAGAGTAAACCTCATTTAT--CAGTCCAAAGGGCAGGGTGTATTATATATATATATA	625
QY	479	AATTTTCTTAAAGAGATTTAATTAATTAATTTAAGTGTGTGATGTTTAATCT--TATCTGT	537
Db	626	TTTTTTTTTAAAAAAGAAACGATATGCAATTAATTTATTTAAGCTTTAAAAACTTATCTC	685
QY	538	CATACATCTCAGTAAGTAATAATGCAAAATCCGTGAGTGTGTTTTT	585
Db	686	CATCAATATCAGTTATTTTAAACTGTAAAGCTTTGTGAGCATTTCTTT	733

RESULT 9
 US-08-927-939-76
 ; Sequence 76, Application US/08927939
 ; Patent No. US2001000640A1
 GENERAL INFORMATION:

```

RESULT 9
US-08-927-939-76
? Sequence 76, Application US/08927939
? Patent No. US20010006640A1
? GENERAL INFORMATION:
? APPLICANT: Grainger, David J.
? APPLICANT: Tatalick, Lauren Marie
? TITLE OF INVENTION: augment an inflammatory response.
? FILE REFERENCE: 295.022051
? CURRENT APPLICATION NUMBER: US/08/927,939
? CURRENT FILING DATE: 1997-09-11
? NUMBER OF SEQ ID NOS: 83
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 76
? LENGTH: 661
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (32)..(331)
? US-08-927-939-76

26.6%; Score 227.8; DB 8; Length 685;
Best Local Similarity 63.8%; Pred. No. 1.8e-33;
Matches 370; Conservative 9; Mismatches 198; Indels 3; Gaps 3

```

26.6%;	Score 227.8;	DB 8;	Length 685;
Best Local Similarity	63.8%;	Pred. No. 1.8e-33;	
Matches 370;	Conservative	9;	Mismatches 198; Indels 3; Gaps 3;
14	TCATCTGAAGCTCACACCTTGGCCCTCCAAAGATGAGAGTTTCTGCTGTGCCC	73	
1	TCCAAGCTGAAGCTCGCATCTTCGCC - TCCAGAGTCAAGATGCTCTCCGCGCTTCTGTGCCC	59	

PRIOR APPLICATION NUMBER: 60/056, 878
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056, 662
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056, 872
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056, 882
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056, 637
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056, 903
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056, 888
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056, 879
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056, 880
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056, 894
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056, 911
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056, 636
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056, 874
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056, 910
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056, 864
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056, 631
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056, 845
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056, 892
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/047, 595
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/057, 761
PRIOR FILING DATE: 05-Sep-1997
PRIOR APPLICATION NUMBER: 60/047, 599
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047, 588
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047, 585
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047, 586
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047, 590
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047, 594
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047, 589
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047, 593
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047, 614
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/043, 578
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043, 576
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/047, 501
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/043, 670
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/056, 632
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056, 664
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056, 876
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056, 881

PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056, 909
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056, 875
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056, 862
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056, 887
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056, 908
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/048, 964
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/057, 650
PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: 60/056, 884
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 280
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 106
LENGTH: 1712

Query Match 26.0%; Score 222.6; DB 9; Length 1712;
Best Local Similarity 68.3%; Pred. No. 2e-32;
Matches 405; Conservative 1; Mismatches 160; Indels 27; Gaps 6;

QY 1 AAACCTTCACCTTCATGCTGAGAGTCACACCCCTTGCCCTCAAGATGAAGTTTCGCA 60
DB 946 AAGATTCATCTCTCAACTGAGAGTCGACCTTCG-CTTCACGATGAAGTTCTTGCC 1004
QY 61 GCGCTTCCTGCTGCTGCTGCTGATGAGCAGCCATTTGAGCCCTGAGGACTTGTGACCA 120
DB 1005 GCGCTTCCTGCTGCTGCTGCTGATGAGCAGCCATTTGAGCCCTGAGGACTTGTGACCA 1064
QY 121 GATTCAGTTCCATTTCCATTCACCTGCTGTTAAGTGATGATAGAAAATTCATC 180
DB 1065 GATTCAGTTCCATTTCCATTCACCTGCTGTTAAGTGATGATAGAAAATTCATC 1124
QY 181 CAGAGGCTGAGAGCTGACCAAGATCACCACATCCATTCACCAAGAGCTGATC 240
DB 1125 CAGAGGCTGAGAGCTGACCAAGATCACCACATCCATTCACCAAGAGCTGATC 1184
QY 241 TTCAGACCAAGAGGAGAGAGTGTGCTGACCCCAAGAGAGATGGTCAGGAT 300
DB 1185 TTCAGACCAAGAGGAGAGAGTGTGCTGACCCCAAGAGAGATGGTCAGGAT 1244
QY 301 TCCATGACATCTGAGCAGCAAAATTTTCAAAATCTGAAGCCATGAGCTTCATACATGA 360
DB 1245 TCCATGACATCTGAGCAGCAAAATTTTCAAAATCTGAAGCCATGAGCTTCATACATGA 1304
QY 361 CTGAGAGTCAAGAGCTTGAAGAAAGCTTATTTTTCCTCAACCTCCAGAGTGCAGT 420
DB 1305 CCA-AGATCTGAGAGCTTGAAGAAAGCTTATTTTTCCTCAACCTCCAGAGTGCAGT 1355
QY 421 GTGACATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 480
DB 1356 GTTATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1399
QY 481 TATTTCTTAAAGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 540
DB 1400 TATGCTTAAAGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1459
QY 541 ACATCTAGTGAATGTAAGATGCAAAATCTGCTGATGCTTTTGTGTTTGTG 593
DB 1460 GG-TACTAGTGTTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1511

RESULT 11
US-09-148-545-106
; sequence 106, Application US/09148545
; Publication No. US20030027132A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

[illegible]

```
EARLIER APPLICATION NUMBER: 60/047,585
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,586
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,590
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,594
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,589
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,593
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,614
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,578
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 280
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 106
LENGTH: 1712
```

Query Match 26.0%; Score 222.6; DB 9; Length 1712;

Best Local Similarity 68.3%; Pred. No. 2e-32; Matches 405; Conservative 1; Mismatches 160; Indels 27; Gaps 6;

```
1 AACCTTCACCTCTCATGTGAGCTCACACCTTGCCCTCCAGATGAGGTTTCTGCA 60
||||| ||| ||||| ||||| ||| ||||| ||||| |||||
946 AACATTCATTTCTCAATCAGAGCTGCACTCTCG-CTTCAGCATTAAGTCTCTCC 1004
||||| ||| ||||| ||||| ||| ||||| ||||| |||||
61 GCGCTTCGTGCTGCTGCTCATGAGGACCACTTTACGCTCCAGGAGCTGCTACGCA 120
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
1005 GCCCTCTGCTGCTGCTCATGAGGACCACTTTACGCTCCAGGAGCTGCTACGCA 1064
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
121 GATTGAGTTTCATTCATCAGCTGCTGCTTTAAGCGATGATAGGAATTCCTATC 180
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
1065 GATGCAATCAATGCCCAAGTCAGCTGCTGATTAATTCACCAATAGGAATCTCAGTG 1124
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
181 CAGAGGCTGAGAGCTCACAGAAATCACCAATCCATGCTCCCAAGAGCTGTGATC 240
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
1125 CAGAGGCTGCGAGACTTATAGAGATCACAGCAGCAAGTGTCCCAAGAGGCTGTGATC 1184
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
241 TTCAGACCAACAGGGGCAAGAGAGTGTGCTGACCCCAAGAGAGATGGTCAAGGAT 300
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
```

```
Db 1185 TTCAGACCATTTGTGGCCAGAGAGATCTGTGACCCCAAGAGAAAGTGTTAGAGAT 1244
QY 301 TCCATGAGCATCTGTGACCAAAATATTTCAAAATCTGAGCCATGACCTTCATATGGA 360
||||| ||| ||||| ||||| ||| ||||| ||||| |||||
Db 1245 TCCATGAGCACCTGAGCAAGCAACCCAACTCCGAGAACTTCACTACTCCACAA 1304
QY 361 CTGAGAGTCAGAGCTTGAGAAAGCTTATTATTTCCCAACCTCCCGCAGGTGCACT 420
| | | | | | | | | | | | | | | | | | | | | | |
Db 1305 CCCA-----AGAACTGACGCTAA---CTTATTTTCCCTGACCTTCCCGACACACCT 1355
QY 421 GTGACATTTATTTTATTAACATCCACAAAGATTTATTAATTAATTTAAAGCATAA 480
| | | | | | | | | | | | | | | | | | | | | | |
Db 1356 GTTTATTTTATTTATTAAT-----GAATTTGTTGTTGATGTGAAACAT-- 1399
QY 481 TATTTCTTAAAGATTTTATTAATTAATTAATTAATTTGATGTTTAACTCTATCTGCAT 540
| | | | | | | | | | | | | | | | | | | | | | |
Db 1400 TATGCTTAAAGTAAGTTAATCTTATTAAGTTATGATGTTTAAAGTTAATCTTCAAT 1459
QY 541 ACATCTTGTGATGATGTAATAATGCAAAATCCTGCTGATGTTTGTGTTTGG 593
| | | | | | | | | | | | | | | | | | | | | | |
Db 1460 GG-TACTAGTGTGTTTGTGATGATGAGAGACTGGGAAATGCTTTCCTCTTG 1511
```

RESULT 12

```
US-09-981-876-105
Sequence 105, Application US/09981876
Patent No. US20020164669A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: P2001P1
CURRENT APPLICATION NUMBER: US/09/981,876
CURRENT FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: 09/148,545
PRIOR FILING DATE: 1998-09-04
PRIOR APPLICATION NUMBER: 60/040,162
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,333
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/038,621
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,161
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,626
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,334
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,336
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,163
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/047,615
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,600
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,597
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,502
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,633
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,583
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,617
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,618
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,503
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,592
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,581
PRIOR FILING DATE: 1997-05-23
```

PRIOR APPLICATION NUMBER: 60/047,584
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,500
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,587
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,492
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,598
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,613
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,582
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,596
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,612
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,569
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,674
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,311
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,671
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,674
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,669
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,312
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,313
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,672
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,315
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/048,974
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/056,886
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,877
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,889
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,893
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,630
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,878
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,662
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,872
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,882
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,637
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,903
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,888
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,879

1	PRIOR FILING DATE: 1997-08-22
2	PRIOR APPLICATION NUMBER: 60/056, 8880
3	PRIOR FILING DATE: 1997-08-22
4	PRIOR APPLICATION NUMBER: 60/056, 8894
5	PRIOR FILING DATE: 1997-08-22
6	PRIOR APPLICATION NUMBER: 60/056, 9111
7	PRIOR FILING DATE: 1997-08-22
8	PRIOR APPLICATION NUMBER: 60/056, 6366
9	PRIOR FILING DATE: 1997-08-22
10	PRIOR APPLICATION NUMBER: 60/056, 874
11	PRIOR FILING DATE: 1997-08-22
12	PRIOR APPLICATION NUMBER: 60/056, 910
13	PRIOR FILING DATE: 1997-08-22
14	PRIOR APPLICATION NUMBER: 60/056, 864
15	PRIOR FILING DATE: 1997-08-22
16	PRIOR APPLICATION NUMBER: 60/056, 6311
17	PRIOR FILING DATE: 1997-08-22
18	PRIOR APPLICATION NUMBER: 60/056, 845
19	PRIOR FILING DATE: 1997-08-22
20	PRIOR APPLICATION NUMBER: 60/056, 8922
21	PRIOR FILING DATE: 1997-08-22
22	PRIOR APPLICATION NUMBER: 60/047, 5585
23	PRIOR FILING DATE: 1997-05-23
24	PRIOR APPLICATION NUMBER: 60/057, 7615
25	PRIOR FILING DATE: 05-Sep-1997
26	PRIOR APPLICATION NUMBER: 60/047, 5599
27	PRIOR FILING DATE: 1997-05-23
28	PRIOR APPLICATION NUMBER: 60/047, 5688
29	PRIOR FILING DATE: 1997-05-23
30	PRIOR APPLICATION NUMBER: 60/047, 5853
31	PRIOR FILING DATE: 1997-05-23
32	PRIOR APPLICATION NUMBER: 60/047, 5666
33	PRIOR FILING DATE: 1997-05-23
34	PRIOR APPLICATION NUMBER: 60/047, 5500
35	PRIOR FILING DATE: 1997-05-23
36	PRIOR APPLICATION NUMBER: 60/047, 5944
37	PRIOR FILING DATE: 1997-05-23
38	PRIOR APPLICATION NUMBER: 60/047, 5689
39	PRIOR FILING DATE: 1997-05-23
40	PRIOR APPLICATION NUMBER: 60/047, 5939
41	PRIOR FILING DATE: 1997-05-23
42	PRIOR APPLICATION NUMBER: 60/047, 6144
43	PRIOR FILING DATE: 1997-05-23
44	PRIOR APPLICATION NUMBER: 60/043, 578
45	PRIOR FILING DATE: 1997-04-11
46	PRIOR APPLICATION NUMBER: 60/043, 576
47	PRIOR FILING DATE: 1997-04-11
48	PRIOR APPLICATION NUMBER: 60/047, 5010
49	PRIOR FILING DATE: 1997-05-23
50	PRIOR APPLICATION NUMBER: 60/043, 670
51	PRIOR FILING DATE: 1997-04-11
52	PRIOR APPLICATION NUMBER: 60/056, 6322
53	PRIOR FILING DATE: 1997-08-22
54	PRIOR APPLICATION NUMBER: 60/056, 6644
55	PRIOR FILING DATE: 1997-08-22
56	PRIOR APPLICATION NUMBER: 60/056, 876
57	PRIOR FILING DATE: 1997-08-22
58	PRIOR APPLICATION NUMBER: 60/056, 8811
59	PRIOR FILING DATE: 1997-08-22
60	PRIOR APPLICATION NUMBER: 60/056, 9099
61	PRIOR FILING DATE: 1997-08-22
62	PRIOR APPLICATION NUMBER: 60/056, 8757
63	PRIOR FILING DATE: 1997-08-22
64	PRIOR APPLICATION NUMBER: 60/056, 8622
65	PRIOR FILING DATE: 1997-08-22
66	PRIOR APPLICATION NUMBER: 60/056, 8877
67	PRIOR FILING DATE: 1997-08-22
68	PRIOR APPLICATION NUMBER: 60/056, 9080
69	PRIOR FILING DATE: 1997-08-22
70	PRIOR APPLICATION NUMBER: 60/048, 9648
71	PRIOR FILING DATE: 1997-06-06
72	PRIOR APPLICATION NUMBER: 60/057, 650
73	PRIOR FILING DATE: 1997-09-05

PRIOR APPLICATION NUMBER: 60/056,884
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 280
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 105
LENGTH: 1822

Query Match 26.08; Score 222.6; DB 9; Length 1822;
Best Local Similarity 68.3%; Pred. No. 2e-32;
Matches 405; Conservative 1; Mismatches 160; Indels 27; Gaps 6;

QY 1 AAACCTTCACCTCTCAGCTGAGCTCAGACCTTGGCCCTCCAGATGAGCTTCTGCA 60
DB 1056 AAACATCCATTTCTCAACAGAGAGCTGCACTCTCG-CTCCACATGAAAGCTCTGCC 1114
QY 61 GCGCTTCGTGCTGCTGCTCATGAGCAGCAGCTTTGAGCCCTCAGAGGACTGCTAGCA 120
DB 1115 GCGCTTCGTGCTGCTGCTCATGAGCAGCAGCTTCAATGCCCAAGGCTGCTAGCA 1174
QY 121 GATTCACTTTCATTCATTCACCTGCTGCTTAACTGATCAATAGGAAATTCCTATTC 180
DB 1175 GATTCATTCATTCATTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1234
QY 181 CAGAGCTGAGAGCTACAGAGATCCAGACCAATCCAAATGCTCCCAAGAGCTGATC 240
DB 1235 CAGAGCTGAGAGCTACAGAGATCCAGACCAATGCTCCCAAGAGAGCTGATC 1294
QY 241 TTCAAGACCAAGGAGGAT 300
DB 1295 TTCAAGACCAATGAGGAT 1354
QY 301 TCCATGAGAGATTCGACCAATATTTTCAAAATGTAAGCAGAGAGCTTCAATACAGGA 360
DB 1355 TCCATGAGAGATTCGACCAATATTTTCAAAATGTAAGCAGAGAGCTTCAATACAGGA 1414
QY 361 CTGAGAGCTGAGAGCTTGAAGAAAGCTTATTTTCCCAAGCTCCCAAGAGAGAGCT 420
DB 1415 CCGA---AGATCTGAGAGTA---CTTATTTTCCCTGAGCTTCCCAAGAGAGAGCT 1465
QY 421 GTGAGATTTATTTATTTATTCATTCACCAAGAGATTTATTTTAAATATTTAAAGCATAA 480
DB 1466 GTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 1509
QY 481 TATTTCTTAAAGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 540
DB 1510 TATGCTTATGATATGATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 1569
QY 541 ACATCTAGTGAATGTAATAATGCAAAATCTGCTGAGAGTGTGTTTGTGTTTG 593
DB 1570 GG-TACTAGTGTGTTTATGATACAGAGACTTGGGGAATGCTTTTCCCTTG 1621

RESULT 13
US-09-148-545-105
Sequence 105, Application US/09148545
Publication No. US20030027132A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: P2001PI
CURRENT APPLICATION NUMBER: US/09/148,545
EARLIER FILING DATE: 1998-09-04
EARLIER APPLICATION NUMBER: PCT/US98/04482
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,161
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626

EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,336
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,163
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,597
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,502
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,633
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,583
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,617
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,618
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,503
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,592
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,581
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,584
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,500
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,587
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,492
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,598
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,613
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,582
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,596
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,612
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,632
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,601
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,580
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,568
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,314
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,569
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,311
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,671
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,674
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,669
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,312
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,313
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,672
EARLIER FILING DATE: 1997-04-11


```
Db 1510 TATGCGCTTAAGTAAATTTCTTATTTAGTATGATGTTTAAAGTTATCTTTCAT 1569
OY 541 ACATCCTAGTGAATGTAAATGCAAAATCCGTGATGTTTGTGTTTGT 593
1570 GC-TACTAGTGTTTTATAGATACAGAGACTTGGGGAATTCCTTCTTG 1621

RESULT 14
US-10-044-090-583
; Sequence 583, Application US/10044090
; Patent No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044,090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 583
; LENGTH: 804
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 452327CB1
US-10-044-090-583

Query Match 25.9%; Score 221.4; DB 12; Length 804;
Best Local Similarity 68.3%; Pred. No. 2.8e-32;
Matches 405; Conservative 0; Mismatches 161; Indels 27; Gaps 6;

OY 1 AAACCTTCACCTCTCATGCTGAGTCAACCTTGCCTCCAGATGAAGTTCTGCA 60
Db 74 AAACATCCAAATTCCTCAAGTGAAGCTGCACCTCTCG-CCTCCAGATGAAGTCTCTGCC 132
OY 61 GCGCTTCTGTGCTGCTGCTCATGTCGACGCACTTTCAGGCTTCAGGAGCTGTCAGCA 120
Db 133 GCGCTTCTGTGCTGCTGCTCATGTCGACGCACTTTCAGGAGCTGTCAGCA 192
OY 121 GATTGAGTTCCATTCATCAATCACTGCTGTTAAAGTGAATGAAGAAATTCCTATC 180
Db 193 GATGCAATCAATGCGCCAGTCACTGCTGTTAACTTCAACCAATGAAGATGATCACTG 252
OY 181 CAGAGGCTGAGAGCTACAGAAATCAACCAATCCATTCCTCCAGAGAGCTGTGTC 240
Db 253 CAGAGGCTGAGAGCTACAGAAATCAACCAATGCTGCTCCAAAGAGCTGTGTC 312
OY 241 TTCAGAGCAAAAGGAGAGAGTGTGCTGACCCCAAGAGAGAGTGGTCAAGAT 300
Db 313 TTCAGAGCAATGTGGCCAAAGAGATCTGTCTACCCCAAGAGAGATGGGTTCAGAT 372
OY 301 TCCATGAGCATCTGACCAAAATTTTCAAAATCTGAAGCATGAGCCTTCATCATGA 360
Db 373 TCCATGAGCATCTGACCAAAAGCAAAATCCGAAGATCTGAAGCATGACCTCCACAA 432
OY 361 CTGAGAGTCAAGAGCTTGAAGAAAGCTTATTTATTTCCCAACCTCCCAAGGTGCA 420
Db 433 CCA--AGAACTCTCAGCTA--CTTATTTTCCCTAGCTTCCCAAGACACCT 483
OY 421 GTGACATTTATTTATTAATCAATCCAAAGAGATTTATTTAAATATTAAGCATAA 480
Db 484 GTTTTATTTATTTATTAAT-----GAATTTTGTGTTGATGTGAACAT-- 527
OY 481 TATTTCTTAAAGATTTATTTATTTATTTAGTGTGATGTTTAACTATCTATCTGTCAT 540
Db 528 TATGCTTAAAGTATTTATTTATTTATTTAGTATGATGTTTAAAGTTATCTTTCAT 587
OY 541 ACATCTAGTGAATGTAAATGCAAAATCCTGTGATGTTGTTTGTGTTTGT 593
Db 588 GG-TACTAGTGTTTTATAGATACAGAGACTTGGGGAATTCCTTCTCTTG 639
```

```
RESULT 15
US-10-044-090-822
; Sequence 822, Application US/10044090
; Patent No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044,090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 822
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 223187CB1
US-10-044-090-822

Query Match 25.6%; Score 218.8; DB 12; Length 600;
Best Local Similarity 75.1%; Pred. No. 7.9e-32;
Matches 302; Conservative 0; Mismatches 92; Indels 8; Gaps 2;

OY 1 AAACCTTCACCTCTCATGCTGAGTCAACCTTGCCTCCAGATGAAGTTCTGCA 60
Db 138 AAACCAACACCTCTCACGCAAGAGCTCACACCTTCAAGCTCCAACTGAAGGTCTCGCA 197
OY 61 GCGCTTCTGTGCTGCTGCTCATGTCGACGCACTTTCAGGCTTCAGGAGCTGTCAGCA 120
Db 198 GCACCTTCTGTGCTGCTGCTCATGTCGACGCTTTCAGGCTTCAGGAGCTGTCAGCA 257
OY 121 GATTGAGTTCCATTCATCAATCACTGCTGTTAAAGTGAATGAAGAAATTCCTATC 180
Db 258 GCTTCTG-----TCCCAACCACTGCTGCTTAACTGCGCAATGGAAGATACCCCTT 311
OY 181 CAGAGGCTGAGAGCTACACAAATCAACCAATCCATTCCTCCAGAGAGCTGTGATC 240
Db 312 CAGGACTAGAGAGCTACAGAAATCAACCAATGCAATGCAAGAGAGCTGTGATC 371
OY 241 TTCAGAGCAAAAGGAGAGAGTGTGCTGACCCCAAGAGAGAGTGGTCAAGAT 300
Db 372 TTCAGAGCAAAAGTGGCAAGAGATATCTGTGCGCAACCCCAAGAGAGTGGGTCAAGAT 431
OY 301 TCCATGAGCATCTGACCAAAATTTTCAAAATCTGAAGCATGAGCCTTCA--TACATG 358
Db 432 TCCATGAGCATCTGACCAAAATTTTCAAAATCTGCAAAAGCCTTAATTAATCACTTTT 491
OY 359 GACTGAGTCAAGAGCTTGAAGAAAGCTTATTTATTTTCCC 400
Db 492 GAAACCAAAAGAGAGCTGAGTGTGCTTAATTTGTTTCCC 533
```

Search completed: February 18, 2003, 03:01:41
Job time : 83 secs